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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:51 ; Search time 31 Seconds
(without alignments)
2040.776 Million cell updates/sec

Title: US-09-934-706-1

Perfect score: 2002
Sequence: 1 MAAYVQPPHPPGHCVTDSGVVYSGVMQWLTQGNKQMLCTCLGNQVSCQETAVTQ 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:
1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep:*
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18: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2002	100.0	343	10	US-09-934-706-1 Sequence 1, Appl
2	1999	99.9	400	10	US-09-934-706-5 Sequence 36, Appl
3	1999	99.9	501	10	US-09-934-706-4 Sequence 132, Appl
4	1988	99.3	2320	12	US-10-279-733-8 Sequence 33, Appl
5	1988	99.3	2355	12	US-10-144-194A-104 Sequence 142, Appl
6	1984	99.1	2386	11	US-09-961-403-1 Sequence 4, Appl
7	1978	98.8	2328	15	US-10-171-311-64 Sequence 104, Appl
8	610	30.5	463	12	US-10-144-194A-52 Sequence 64, Appl
9	382.5	19.1	660	9	US-09-801-196-35 Sequence 52, Appl
10	382.5	19.1	660	12	US-10-153-185-14 Sequence 14, Appl
11	382.5	19.1	660	12	US-10-301-822-125 Sequence 125, Appl
12	382.5	19.1	660	12	US-10-219-561-14 Sequence 1, Appl
13	382.5	19.1	660	12	US-10-131-985-25 Sequence 25, Appl
14	382.5	19.1	660	15	US-10-219-329-14 Sequence 14, Appl
15	382.5	19.1	663	12	US-10-115-223-30 Sequence 30, Appl

16	380	19.0	429	12	US-10-115-223-45 Sequence 45, Appl
17	374	18.7	707	9	US-09-801-196-36 Sequence 36, Appl
18	374	18.7	707	12	US-10-301-822-132 Sequence 132, Appl
19	374	18.7	707	12	US-10-131-985-33 Sequence 33, Appl
20	374	18.7	707	11	US-10-171-311-142 Sequence 4, Appl
21	356.5	17.8	259	15	US-09-940-235-4 Sequence 1270, Appl
22	242	12.1	164	9	US-09-925-301-1270 Sequence 62, Appl
23	235.5	11.8	793	15	US-10-171-311-62 Sequence 548, Appl
24	229	11.4	231	9	US-09-925-302-548 Sequence 40316, A
25	205	10.2	57	9	US-09-864-761-40316 Sequence 1738, Ap
26	193.5	9.7	1479	15	US-10-015-218-1738 Sequence 1739, Ap
27	193.5	9.7	1479	15	US-10-015-218-1739 Sequence 95, Appl
28	193	9.6	1456	10	US-09-870-759-95 Sequence 95, Appl
29	193	9.6	1456	12	US-09-751-708A-95 Sequence 115, Appl
30	170	8.5	301	9	US-09-989-722-115 Sequence 115, Appl
31	170	8.5	301	9	US-09-989-723-115 Sequence 115, Appl
32	170	8.5	301	9	US-09-989-727-115 Sequence 115, Appl
33	170	8.5	301	9	US-09-989-727-115 Sequence 115, Appl
34	170	8.5	301	10	US-09-989-731-115 Sequence 115, Appl
35	170	8.5	301	10	US-09-989-733-115 Sequence 115, Appl
36	170	8.5	301	10	US-09-991-072-115 Sequence 115, Appl
37	170	8.5	301	10	US-09-990-442-115 Sequence 115, Appl
38	170	8.5	301	10	US-09-991-163-115 Sequence 115, Appl
39	170	8.5	301	10	US-09-993-604-115 Sequence 115, Appl
40	170	8.5	301	10	US-09-990-456-115 Sequence 115, Appl
41	170	8.5	301	10	US-09-989-721-115 Sequence 115, Appl
42	170	8.5	301	10	US-09-992-598-115 Sequence 115, Appl
43	170	8.5	301	10	US-09-989-293A-115 Sequence 115, Appl
44	170	8.5	301	10	US-09-989-735-115 Sequence 115, Appl
45	170	8.5	301	10	US-09-990-444-115 Sequence 115, Appl

ALIGNMENTS

RESULT 1
US-09-934-706-1
; Sequence 1, Application US/09934706
; Patent No. US20020102709A1
; GENERAL INFORMATION:
; APPLICANT: Tercumo Corporation
; TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
; FILE REFERENCE: 19990120
; CURRENT APPLICATION NUMBER: US/09/934, 706
; CURRENT FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE:
; SEQ ID NO 1
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified Human
; OTHER INFORMATION: Fibronectin Collagen-Binding Domain
; NAME/KEY: INIT_MET
; LOCATION: (1)
; NAME/KEY: DOMAIN
; LOCATION: (2..341)
; OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
; NAME/KEY: CONFLICT
; LOCATION: (69)
; NAME/KEY: CONFLICT
; LOCATION: (125)
; LOCATION: (125)
; US-09-934-706-1

Query Match 100.0%; Score 2002; DB 10; Length 343;
Best Local Similarity 100.0%; Pred No. 6.6e-179;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAYVQPPHPPGHCVTDSGVVYSGVMQWLTQGNKQMLCTCLGNQVSCQETAVTQ 60
DB 1 MAAYVQPPHPPGHCVTDSGVVYSGVMQWLTQGNKQMLCTCLGNQVSCQETAVTQ 60

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QY 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNYEDQKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNYEDQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLVNNHNYTDCISEGRDNMKKCGTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDCISEGRDNMKKCGTTONYADQKFGFCPMAAHEI 180
QY 121 TRGNSNGALCHFPFLVNNHNYTDCISEGRDNMKKCGTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDCISEGRDNMKKCGTTONYADQKFGFCPMAAHEI 180
QY 181 CTTEGVMYRIGDQMDKHMDGMMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVYVND 240
DB 181 CTTEGVMYRIGDQMDKHMDGMMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVYVND 240
QY 241 TFHRRHEGHMLNCTCGGQGRGKCDPVDCODSEGTFTYQIGDSWEKTVHGVRYOCYC 300
DB 241 TFHRRHEGHMLNCTCGGQGRGKCDPVDCODSEGTFTYQIGDSWEKTVHGVRYOCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQNSHPIDMLE 343
DB 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQNSHPIDMLE 343
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RESULT 2

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US-09-934-706-5
; Sequence 5, Application US/09934706
; Patent No. US20020102709A1
; GENERAL INFORMATION:
; APPLICANT: Terumo Corporation
; TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 19990120
; CURRENT APPLICATION NUMBER: US/09/934.706
; CURRENT FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE:
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Hybrid
; OTHER INFORMATION: Polypeptide of Human Fibronectin Collagen-Binding
; OTHER INFORMATION: Domain and Human Epidermal Growth Factor
; NAME/KEY: INIT _MET
; LOCATION: (1)
; NAME/KEY: DOMAIN
; LOCATION: (2)..(341)
; OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
; NAME/KEY: PEPTIDE
; LOCATION: (343)..(347)
; OTHER INFORMATION: /note="enterokinas recognition sequence"
; NAME/KEY: PEPTIDE
; LOCATION: (348)..(400)
; OTHER INFORMATION: /note="human epidermal growth factor"
US-09-934-706-5
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Query Match 99.9%; Score 1999; DB 10; Length 400;
Best Local Similarity 99.7%; Pred. No.1.5e-178;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAAYVQPPHPQPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
DB 1 MAAYVQPPHPQPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNYEDQKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNYEDQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLVNNHNYTDCISEGRDNMKKCGTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDCISEGRDNMKKCGTTONYADQKFGFCPMAAHEI 180
QY 181 CTTEGVMYRIGDQMDKHMDGMMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVYVND 240
DB 181 CTTEGVMYRIGDQMDKHMDGMMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVYVND 240
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DB 181 CTTEGVMYRIGDQMDKHMDGMMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVYVND 240
QY 241 TFHRRHEGHMLNCTCGGQGRGKCDPVDCODSEGTFTYQIGDSWEKTVHGVRYOCYC 300
DB 241 TFHRRHEGHMLNCTCGGQGRGKCDPVDCODSEGTFTYQIGDSWEKTVHGVRYOCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQNSHPIDMLE 343
DB 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQNSHPIDMLE 343
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RESULT 3

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US-09-934-706-4
; Sequence 4, Application US/09934706
; Patent No. US20020102709A1
; GENERAL INFORMATION:
; APPLICANT: Terumo Corporation
; TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 19990120
; CURRENT APPLICATION NUMBER: US/09/934.706
; CURRENT FILING DATE: 2001-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE:
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Hybrid
; OTHER INFORMATION: Polypeptide of Human Fibronectin Collagen-Binding
; OTHER INFORMATION: Domain and Human Basic Fibroblast Growth Factor
; NAME/KEY: INIT _MET
; LOCATION: (1)
; NAME/KEY: DOMAIN
; LOCATION: (2)..(341)
; OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
; NAME/KEY: PEPTIDE
; LOCATION: (343)..(347)
; OTHER INFORMATION: /note="enterokinas recognition sequence"
; NAME/KEY: PEPTIDE
; LOCATION: (348)..(501)
; OTHER INFORMATION: /note="human fibroblast growth factor"
US-09-934-706-4
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Query Match 99.9%; Score 1999; DB 10; Length 501;
Best Local Similarity 99.7%; Pred. No.2e-178;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MAAYVQPPHPQPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
DB 1 MAAYVQPPHPQPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNYEDQKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCCTTEGRDGHLMCTTSNYEDQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLVNNHNYTDCISEGRDNMKKCGTTONYADQKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHFPFLVNNHNYTDCISEGRDNMKKCGTTONYADQKFGFCPMAAHEI 180
QY 181 CTTEGVMYRIGDQMDKHMDGMMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVYVND 240
DB 181 CTTEGVMYRIGDQMDKHMDGMMRCTCVANGRGEMWTCLAYSQLRDQCIYDDITVYVND 240
QY 241 TFHRRHEGHMLNCTCGGQGRGKCDPVDCODSEGTFTYQIGDSWEKTVHGVRYOCYC 300
DB 241 TFHRRHEGHMLNCTCGGQGRGKCDPVDCODSEGTFTYQIGDSWEKTVHGVRYOCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQNSHPIDMLE 343
DB 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTETPSQNSHPIDMLE 343
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RESULT 4

US-10-279-733-8
Sequence 8, Application US/10279733
Publication No. US20030194400A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Liu, Cheng
APPLICANT: Bagington, Thomas, S.
TITLE OF INVENTION: Targeted Thrombosis
FILE REFERENCE: 1361.016W01
CURRENT APPLICATION NUMBER: US/10/279,733
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 60/336331
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 2320
TYPE: PRT
ORGANISM: Homo sapiens
US-10-279-733-8

Query Match 99.3%; Score 1988; DB 12; Length 2320;
Best Local Similarity 100.0%; Pred. No. 1.4e-176;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAYYQPPHPQPPYGHCTVDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
DB 256 AAYYQPPHPQPPYGHCTVDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 315
QY 62 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCTTSNRYDQDKYSCFCTHTVLVQT 121
DB 316 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCTTSNRYDQDKYSCFCTHTVLVQT 375
QY 122 RGNNSGALCHFPFLYNNHNYTDCSEGRDNMKCGTTONYADADQKFGFCPMAAHEIC 181
DB 376 RGNNSGALCHFPFLYNNHNYTDCSEGRDNMKCGTTONYADADQKFGFCPMAAHEIC 435
QY 182 TTNEGVMYRIGDQMDQKHMGHMRCTCVNGRGEMWTCIAYSQLRQCIYDDITVYVNDT 241
DB 436 TTNEGVMYRIGDQMDQKHMGHMRCTCVNGRGEMWTCIAYSQLRQCIYDDITVYVNDT 495
QY 242 FHKRHEGHMLNCTCGGGRGKWCDPVDCODESETGTFTYQIGDSMEKYVHGVRVYCCYCY 301
DB 496 FHKRHEGHMLNCTCGGGRGKWCDPVDCODESETGTFTYQIGDSMEKYVHGVRVYCCYCY 555
QY 302 GRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIOW 341
DB 556 GRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIOW 595

RESULT 5

US-10-144-194A-104
Sequence 104, Application US/10144194A
Publication No. US20030215809A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer Genes
FILE REFERENCE: 3U 103 R1
CURRENT APPLICATION NUMBER: US/10/144,194A
CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn version 3.0
SEQ ID NO 104
LENGTH: 2355
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-194A-104

Query Match 99.3%; Score 1988; DB 12; Length 2355;
Best Local Similarity 100.0%; Pred. No. 1.4e-176;

Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAYYQPPHPQPPYGHCTVDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
DB 291 AAYYQPPHPQPPYGHCTVDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 350
QY 62 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCTTSNRYDQDKYSCFCTHTVLVQT 121
DB 351 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCTTSNRYDQDKYSCFCTHTVLVQT 410
QY 122 RGNNSGALCHFPFLYNNHNYTDCSEGRDNMKCGTTONYADADQKFGFCPMAAHEIC 181
DB 411 RGNNSGALCHFPFLYNNHNYTDCSEGRDNMKCGTTONYADADQKFGFCPMAAHEIC 470
QY 182 TTNEGVMYRIGDQMDQKHMGHMRCTCVNGRGEMWTCIAYSQLRQCIYDDITVYVNDT 241
DB 471 TTNEGVMYRIGDQMDQKHMGHMRCTCVNGRGEMWTCIAYSQLRQCIYDDITVYVNDT 530
QY 242 FHKRHEGHMLNCTCGGGRGKWCDPVDCODESETGTFTYQIGDSMEKYVHGVRVYCCYCY 301
DB 531 FHKRHEGHMLNCTCGGGRGKWCDPVDCODESETGTFTYQIGDSMEKYVHGVRVYCCYCY 590
QY 302 GRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIOW 341
DB 591 GRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIOW 630

Query Match 99.1%; Score 1984; DB 11; Length 2386;
Best Local Similarity 99.7%; Pred. No. 3.3e-176;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAYYQPPHPQPPYGHCTVDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
DB 291 AAYYQPPHPQPPYGHCTVDSGVVSVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 350
QY 62 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCTTSNRYDQDKYSCFCTHTVLVQT 121
DB 351 YGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCTTSNRYDQDKYSCFCTHTVLVQT 410
QY 122 RGNNSGALCHFPFLYNNHNYTDCSEGRDNMKCGTTONYADADQKFGFCPMAAHEIC 181
DB 411 RGNNSGALCHFPFLYNNHNYTDCSEGRDNMKCGTTONYADADQKFGFCPMAAHEIC 470
QY 182 TTNEGVMYRIGDQMDQKHMGHMRCTCVNGRGEMWTCIAYSQLRQCIYDDITVYVNDT 241
DB 471 TTNEGVMYRIGDQMDQKHMGHMRCTCVNGRGEMWTCIAYSQLRQCIYDDITVYVNDT 530
QY 242 FHKRHEGHMLNCTCGGGRGKWCDPVDCODESETGTFTYQIGDSMEKYVHGVRVYCCYCY 301
DB 531 FHKRHEGHMLNCTCGGGRGKWCDPVDCODESETGTFTYQIGDSMEKYVHGVRVYCCYCY 590

Db 531 FHKEHBEHMLNCTCFQGRGKMKCDPVDCQDSEGTFTFYQIGDSWEKXVHGVRXQCYCY 590
Qy 302 GRGIGEMHCOPLOQTYPPSSSGVEVFITETTPSQPNSHPIQW 341
Db 591 GRGIGEMHCOPLOQTYPPSSSGVEVFITETTPSQPNSHPIQW 630

RESULT 7

US-10-171-311-64
Sequence 64, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoerish, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64
LENGTH: 2328
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-64

Query Match 98.8%, Score 1978, DB 15, Length 2328;
Best Local Similarity 99.4%, Pred. No. 1.2e-175;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 AAVYQPPHPPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNVSCQETAVTQT 61
Db 264 AAVYQPPHPPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNVSCQETAVTQT 323
Qy 62 YGNSNGEPCVLPPTVNGRTFTYSCCTEGRODGHLMCSTTSNYEDQKYSFCTDHTVLVOT 121
Db 324 YGNSNGEPCVLPPTVNGRTFTYSCCTEGRODGHLMCSTTSNYEDQKYSFCTDHTVLVOT 383
Qy 122 RGSNSNGLCHFPFLYNNHNTDCTSEGRBDNMKCGTTONYVADQKGFCEMAHEIIC 181
Db 384 QGSNSNGLCHFPFLYNNHNTDCTSEGRBDNMKCGTTONYVADQKGFCEMAHEIIC 443
Qy 182 TTNGVWVRIDQMDKQDMGHMRCCTCVNGRGEMTCTIAYSQLRDQCIYDITVYVNDT 241
Db 444 TTNGVWVRIDQMDKQDMGHMRCCTCVNGRGEMTCTIAYSQLRDQCIYDITVYVNDT 503
Qy 242 FHKEHBEHMLNCTCFQGRGKMKCDPVDCQDSEGTFTFYQIGDSWEKXVHGVRXQCYCY 301
Db 504 FHKEHBEHMLNCTCFQGRGKMKCDPVDCQDSEGTFTFYQIGDSWEKXVHGVRXQCYCY 563
Qy 302 GRGIGEMHCOPLOQTYPPSSSGVEVFITETTPSQPNSHPIQW 341
Db 564 GRGIGEMHCOPLOQTYPPSSSGVEVFITETTPSQPNSHPIQW 603

RESULT 8

US-10-144-194A-52
Sequence 52, Application US/10144194A
Publication No. US20030215809A1

GENERAL INFORMATION:
APPLICANT: Origene Technologies Inc
TITLE OF INVENTION: Regulated Breast Cancer Genes
FILE REFERENCE: 3U 103 R1
CURRENT APPLICATION NUMBER: US/10/144,194A
CURRENT FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn version 3.0
SEQ ID NO 52
LENGTH: 463
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-194A-52

Query Match 30.5%, Score 610, DB 12, Length 463;
Best Local Similarity 99.1%, Pred. No. 1.3e-48;
Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAVYQPPHPPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNVSCQETAVTQT 61
Db 327 AAVYQPPHPPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNVSCQETAVTQT 386
Qy 62 YGNSNGEPCVLPPTVNGRTFTYSCCTEGRODGHLMCSTTSNYEDQKYSFCTDHTVLVOT 108
Db 387 YGNSNGEPCVLPPTVNGRTFTYSCCTEGRODGHLMCSTTSNYEDQKYSFCTDHTVLVOT 433

RESULT 9

US-09-801-196-35
Sequence 35, Application US/09801196
Patent No. US20020037827A1
GENERAL INFORMATION:
APPLICANT: Wang, Kai
APPLICANT: Smith, Ryan
APPLICANT: Fajardo, Mark
APPLICANT: Moss, Patrick
TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
FILE REFERENCE: 240083.509
CURRENT APPLICATION NUMBER: US/09/801,196
CURRENT FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-09-801-196-35

Query Match 19.1%, Score 382.5, DB 9, Length 660;
Best Local Similarity 38.3%, Pred. No. 3.5e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

Qy 55 ETAVTQTYGNSNGEPCVLPPTVNGRTFTYSCCTEGRODGHLMCSTTSNYEDQKYSFCTD 114
Db 217 EGAVVAVKYNSADGEYCKFPFLFNKGKYNSTCTGSDGLMCSITVNFEXDKGYGFC-P 275
Qy 115 HTVAVQVRGNSNGLCHFPFLYNNHNTDCTSEGRBDNMKCGTTONYVADQKGFCEPM 174
Db 276 HEALF-TWGNNAABQPKCFPFRTGTSYDSCCTEGRTDGYRWCGTIEDYDRDKKXGFCPE 334
Qy 175 AAHEICTTNEGV-----MYRIGDQMDKQDMGHMRCCTCVNGRGEMTCTIAYSQLR 226
Db 335 TAWSTVGSNGBGACVAPFTFLNKKYSS-----CTAAGNSDGMWCAATTANYVDDDR 385
Qy 227 DQCIYDITVYVNDTFHKEHBEHML 252
Db 386 KWGFCPDGYSL--FLVAHAHEFGHAM 409

RESULT 10

US-10-153-185-14
Sequence 14, Application US/10153185

```
Publication No. US20030148959A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Malik, Sohail
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REFERENCE: 1443.034US1
CURRENT APPLICATION NUMBER: US/10/153,185
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-185-14

Query Match
Best Local Similarity 19.1%; Score 382.5; DB 12; Length 660;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

55 ETAVTQYGGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYPQDQKYSFCTD 114
217 EGVAVKVKGNADGECCKPFLFNKGKYNSTCTDGTGSDGLMSTTYNFEKDKYGC-P 275
115 HTVLVOTRGNSNGALCHPFLYNNHNYDCTSEGRDNMKWCCTTQNYDADQKFGFCPM 174
276 HEALF-TMGNAEGOCCKPFFRQGTSYSDCTTEGRTDGYRMCGTTEDYDRDKYGCPE 334
175 AAHEEICTTNEGV-----MYRIDQMDKQDHMGHMRCTCVNGRGEGWTCIA---YSQLR 226
335 TAWSTVGNSGAPCVFPFTFLGNKYES-----CTSAGRSDDKMCWATTANYDDDR 385
227 DQCIVDITVNVNDTFHKRHEEGHML 252
386 KMGFCPDQGYSL--FLVAHAEFGHAM 409

RESULT 11
US-10-301-822-125
Sequence 125, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangl
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MEMO1-029P22NM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 125
LENGTH: 660
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-301-822-125
```

```
Query Match
Best Local Similarity 19.1%; Score 382.5; DB 12; Length 660;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

55 ETAVTQYGGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYPQDQKYSFCTD 114
217 EGVAVKVKGNADGECCKPFLFNKGKYNSTCTDGTGSDGLMSTTYNFEKDKYGC-P 275
115 HTVLVOTRGNSNGALCHPFLYNNHNYDCTSEGRDNMKWCCTTQNYDADQKFGFCPM 174
276 HEALF-TMGNAEGOCCKPFFRQGTSYSDCTTEGRTDGYRMCGTTEDYDRDKYGCPE 334
175 AAHEEICTTNEGV-----MYRIDQMDKQDHMGHMRCTCVNGRGEGWTCIA---YSQLR 226
335 TAWSTVGNSGAPCVFPFTFLGNKYES-----CTSAGRSDDKMCWATTANYDDDR 385
227 DQCIVDITVNVNDTFHKRHEEGHML 252
386 KMGFCPDQGYSL--FLVAHAEFGHAM 409

RESULT 12
US-10-219-561-14
Sequence 14, Application US/10219561
Publication No. US20030166567A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Malik, Sohail
APPLICANT: Villanueva, Julie M.
TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
FILE REFERENCE: 1443.008US2
CURRENT APPLICATION NUMBER: US/10/219,561
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 10/032,376
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 10/153,185
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/312,726
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-561-14

Query Match
Best Local Similarity 19.1%; Score 382.5; DB 12; Length 660;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

55 ETAVTQYGGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYPQDQKYSFCTD 114
217 EGVAVKVKGNADGECCKPFLFNKGKYNSTCTDGTGSDGLMSTTYNFEKDKYGC-P 275
115 HTVLVOTRGNSNGALCHPFLYNNHNYDCTSEGRDNMKWCCTTQNYDADQKFGFCPM 174
276 HEALF-TMGNAEGOCCKPFFRQGTSYSDCTTEGRTDGYRMCGTTEDYDRDKYGCPE 334
175 AAHEEICTTNEGV-----MYRIDQMDKQDHMGHMRCTCVNGRGEGWTCIA---YSQLR 226
335 TAWSTVGNSGAPCVFPFTFLGNKYES-----CTSAGRSDDKMCWATTANYDDDR 385
227 DQCIVDITVNVNDTFHKRHEEGHML 252
386 KMGFCPDQGYSL--FLVAHAEFGHAM 409

RESULT 13
US-10-131-985-25
Sequence 25, Application US/10131985
Publication No. US20030199440A1
```

```

GENERAL INFORMATION:
APPLICANT: Dack, Kevin N
APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
APPLICANT: Occleston, Nicholas L
TITLE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT FILING DATE: 2002-04-25
PRIORITY FILING DATE: 2000-11-30
PRIORITY FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-985-25

```

```

Query Match 19.1%; Score 382.5; DB 12; Length 660;
Best Local Similarity 38.3%; Pred. No. 3.5e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

QY 55 ETAVTQTGGNSNGPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTD 114
DB 217 EGQVVRKYGNADGEYCKFPFLYNNHNYTDCTSEGRDNMKWCGTTONYADOKFGFCPM 174
QY 115 HTVLVOTRGNSNGALCHFPFLYNNHNYTDCTSEGRDNMKWCGTTONYADOKFGFCPM 174
DB 276 HEALF-TMGNAEBOQPKFPFRFGTSYDCTTEGRTDGYRWCGTTEDYDRDKKYGFCPE 334
QY 175 AAHEICTTNGV-----MYRIDQMDKOHMGHMRCTCVNGRGEMTCTIA---YSQLR 226
DB 335 TAMSTVGNSGACVCPFPFTFLGNKYES-----CTSAGRSDGKWCATTANYDDDR 385
QY 227 DQCIVDITVYVNDTFHKKHEGHML 252
DB 386 KWGFCPDGYSL--FLVAHAEFGHAM 409

```

```

RESULT 14
US-10-219-329-14
Sequence 14, Application US/10219329
Publication No. US20030096757A1
GENERAL INFORMATION:
APPLICANT: Quirk, Stephen
APPLICANT: Weart, Ilona F.
TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
FILE REFERENCE: 1443.035M01
CURRENT FILING DATE: 2002-08-15
PRIORITY FILING DATE: 2000-12-21
PRIORITY FILING DATE: 2001-12-21
PRIORITY FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-10-219-329-14

```

```

Query Match 19.1%; Score 382.5; DB 15; Length 660;
Best Local Similarity 38.3%; Pred. No. 3.5e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

QY 55 ETAVTQTGGNSNGPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTD 114

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DB 217 EGQVVRKYGNADGEYCKFPFLYNNHNYTDCTSEGRDNMKWCGTTONYADOKFGFCPM 174
QY 115 HTVLVOTRGNSNGALCHFPFLYNNHNYTDCTSEGRDNMKWCGTTONYADOKFGFCPM 174
DB 276 HEALF-TMGNAEBOQPKFPFRFGTSYDCTTEGRTDGYRWCGTTEDYDRDKKYGFCPE 334
QY 175 AAHEICTTNGV-----MYRIDQMDKOHMGHMRCTCVNGRGEMTCTIA---YSQLR 226
DB 335 TAMSTVGNSGACVCPFPFTFLGNKYES-----CTSAGRSDGKWCATTANYDDDR 385
QY 227 DQCIVDITVYVNDTFHKKHEGHML 252
DB 386 KWGFCPDGYSL--FLVAHAEFGHAM 409

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RESULT 15
US-10-115-223-30
Sequence 30, Application US/10115223
Publication No. US20030176334A1
GENERAL INFORMATION:
APPLICANT: Cheresch, David A.
APPLICANT: Brooks, Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
FILE REFERENCE: MER00495
CURRENT FILING DATE: 2002-04-02
PRIORITY FILING DATE: 1999-03-23
PRIORITY FILING DATE: 1996-05-31
PRIORITY FILING DATE: 1996-05-31
PRIORITY FILING DATE: 1996-05-31
PRIORITY FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 663
TYPE: PRT
ORGANISM: Gallus gallus
US-10-115-223-30

```

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Query Match 19.1%; Score 382.5; DB 12; Length 663;
Best Local Similarity 37.0%; Pred. No. 3.6e-27;
Matches 77; Conservative 31; Mismatches 75; Indels 25; Gaps 6;

QY 55 ETAVTQTGGNSNGPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTD 114
DB 214 EGQVVRKYGNADGEYCKFPFLYNNHNYTDCTSEGRDNMKWCGTTONYADOKFGFCPM 174
QY 115 HTVLVOTRGNSNGALCHFPFLYNNHNYTDCTSEGRDNMKWCGTTONYADOKFGFCPM 174
DB 274 ESLE-TMGNGDQPKFPFRFGTSYDCTTEGRTDGYRWCGTTEDYDRDKKYGFCPE 331
QY 175 AAHEICTTNGV-----MYRIDQMDKOHMGHMRCTCVNGRGEMTCTIA---YSQLR 228
DB 332 TAMSTVGNSGACVCPFPFTFLGNKYDS-----CTSAGRSDGKWCATTANYDDDR 382
QY 229 ----CTVDITVYVNDTFHKKHEGHML 252
DB 383 KWGFC--PDGYSL--FLVAHAEFGHAM 406

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Search completed: November 28, 2003, 15:03:26
Job time : 32 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:11 ; Search time 21 Seconds
(without alignments)
691.077 Million cell updates/sec

Title: US-09-934-706-1

Perfect score: 2002
Sequence: 1 MAAYVQPPHPPPYGHCV.....EVFTETTPQNSHPQMLE 343

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1979	98.9	2386	2	US-09-016-366A-12
2	1978	98.8	2446	2	US-08-551-356-2
3	1978	98.8	2446	5	PCT-US93-12687-2
4	1973	98.6	2337	6	545158-1
5	1971	98.5	2334	1	US-08-283-857-1
6	1971	98.5	2334	5	PCT-US95-09819-1
7	1959	97.9	2231	1	US-08-153-799-16
8	382.5	19.1	631	3	US-08-448-489-17
9	382.5	19.1	660	4	US-08-704-711A-18
10	382.5	19.1	660	4	US-09-521-220-18
11	382.5	19.1	660	4	US-09-381-104-19
12	382.5	19.1	660	4	US-09-194-468A-30
13	380	19.0	429	4	US-09-194-468A-45
14	374	18.7	707	3	US-08-704-711A-19
15	374	18.7	707	4	US-09-521-220-19
16	374	18.7	707	4	US-09-391-104-20
17	374	18.7	708	3	US-08-448-489-16
18	371	18.5	65	2	US-08-982-597A-19
19	371	18.5	65	3	US-09-136-218-19
20	348	17.4	60	2	US-08-982-597A-18
21	348	17.4	60	3	US-09-136-218-18
22	290	14.5	48	2	US-08-982-597A-22
23	290	14.5	48	3	US-09-136-218-22
24	278	13.9	48	2	US-08-982-597A-20
25	278	13.9	48	3	US-09-136-218-20
26	258	12.9	43	2	US-08-982-597A-21
27	258	12.9	43	3	US-09-136-218-21

28	243	12.1	474	2	US-08-836-854-9	Sequence 9, Appl
29	239.5	12.0	422	2	US-08-836-854-12	Sequence 12, Appl
30	232	11.6	188	1	US-08-142-448B-14	Sequence 14, Appl
31	206	10.3	37	2	US-08-982-597A-17	Sequence 17, Appl
32	206	10.3	37	3	US-09-136-218-17	Sequence 17, Appl
33	202	10.1	1455	3	US-08-840-062-5	Sequence 5, Appl
34	195.5	9.8	1463	1	US-08-220-603A-11	Sequence 11, Appl
35	193.5	9.7	1479	3	US-08-840-062-4	Sequence 4, Appl
36	187	9.3	1479	3	US-08-840-062-2	Sequence 2, Appl
37	180.5	9.0	1487	3	US-08-840-062-7	Sequence 7, Appl
38	170	8.5	301	4	US-09-996-243-115	Sequence 115, App
39	170	8.5	655	1	US-08-148-910-12	Sequence 12, Appl
40	170	8.5	655	1	US-08-448-937A-12	Sequence 12, Appl
41	143	7.1	1722	4	US-09-194-612A-1	Sequence 1, Appl
42	140.5	7.0	1449	3	US-08-840-062-6	Sequence 6, Appl
43	140.5	7.0	1723	4	US-09-194-612A-31	Sequence 31, Appl
44	130	6.5	24	2	US-08-982-597A-23	Sequence 23, Appl
45	130	6.5	24	3	US-09-136-218-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-016-366A-12
Sequence 12, Application US/09016366A

Patent No. 5955431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

APPLICANT: Huang, Chifu

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,366A

FILING DATE: January 30, 1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,090

FILING DATE: 05-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7093

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 2386 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-016-366A-12

Query Match 98.9%; Score 1979; DB 2; Length 2386;
Best Local Similarity 99.4%; Pred. No. 9,4e-175;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 350
QY 62 YGNSNGBPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNVEDOKYSFCTDHTVLVQT 121
DB 351 YGNSNGBPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNVEDOKYSFCTDHTVLVQT 410
QY 122 RGNNSGALCHFPPLVNNHNYTDCSTSEGRDNMKCGTTONYVDADOKFGFCPMAAHERIC 181
DB 411 QGNSNGALCHFPPLVNNHNYTDCSTSEGRDNMKCGTTONYVDADOKFGFCPMAAHERIC 470
QY 182 TTNGVWYRIDDQMDKHDMGMMRCTCVNGRGEMTCIAYSQLRDQCIYVDITVNVDT 241
DB 471 TTNGVWYRIDDQMDKHDMGMMRCTCVNGRGEMTCIAYSQLRDQCIYVDITVNVDT 530
QY 242 FHKHEBGMHMLNCTCFQGRGRMKCDPVDOCDSEGTGYOIGSWEXYVGVYQCCY 301
DB 531 FHKHEBGMHMLNCTCFQGRGRMKCDPVDOCDSEGTGYOIGSWEXYVGVYQCCY 590
QY 302 GRGIGEMHCQPLQTYPSSSGPEVEVFTETPSQPNSHPIQW 341
DB 591 GRGIGEMHCQPLQTYPSSSGPEVEVFTETPSQPNSHPIQW 630

RESULT 2

US-08-551-356-2
; Sequence 2, Application US/08551356
; Patent No. 5830700
; GENERAL INFORMATION:
; APPLICANT: Iranl, Meher H.
; TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/551,356
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,762
; FILING DATE:
; APPLICATION NUMBER: US/07/998,271
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Holly, Julie A
; REGISTRATION NUMBER: 33-246
; REFERENCE/DOCKET NUMBER: 92-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2446 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-551-356-2

Query Match 98.8%; Score 1978; DB 2; Length 2446;
Best Local Similarity 99.4%; Pred. No. 1.2e-174;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 350
QY 62 YGNSNGBPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNVEDOKYSFCTDHTVLVQT 121
DB 351 YGNSNGBPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNVEDOKYSFCTDHTVLVQT 410
QY 122 RGNNSGALCHFPPLVNNHNYTDCSTSEGRDNMKCGTTONYVDADOKFGFCPMAAHERIC 181
DB 411 QGNSNGALCHFPPLVNNHNYTDCSTSEGRDNMKCGTTONYVDADOKFGFCPMAAHERIC 470
QY 182 TTNGVWYRIDDQMDKHDMGMMRCTCVNGRGEMTCIAYSQLRDQCIYVDITVNVDT 241
DB 471 TTNGVWYRIDDQMDKHDMGMMRCTCVNGRGEMTCIAYSQLRDQCIYVDITVNVDT 530
QY 242 FHKHEBGMHMLNCTCFQGRGRMKCDPVDOCDSEGTGYOIGSWEXYVGVYQCCY 301
DB 531 FHKHEBGMHMLNCTCFQGRGRMKCDPVDOCDSEGTGYOIGSWEXYVGVYQCCY 590
QY 302 GRGIGEMHCQPLQTYPSSSGPEVEVFTETPSQPNSHPIQW 341
DB 591 GRGIGEMHCQPLQTYPSSSGPEVEVFTETPSQPNSHPIQW 630

RESULT 3

PCT-US93-12687-2
; Sequence 2, Application PC/TUS9312687
; GENERAL INFORMATION:
; APPLICANT: Iranl, Meher H.
; TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12687
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/998,271
; FILING DATE: 31-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-648
; REFERENCE/DOCKET NUMBER: 92-26PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2446 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-12687-2

Query Match 98.8%; Score 1978; DB 5; Length 2446;
Best Local Similarity 99.4%; Pred. No. 1.2e-174;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 291 AAVYQOPHPQPPYGHCVTDSGVVYSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT 350

QY 62 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSTSNYEODOKYSECTDHTVLVOT 121
| | | | |
Db 351 YGNSLNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSTSNYEODOKYSECTDHTVLVOT 410
| | | | |
QY 122 RGSNSGALCHFPFLYNNHNYTDCSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 181
| | | | |
Db 411 OGNSNGALCHFPFLYNNHNYTDCSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 470
| | | | |
QY 182 TTNEGVYRIGDQMDKQHDGMMRCTCVNGRGEMWTCIAYSQLRDQCIYDDITTYVNDT 241
| | | | |
Db 471 TTNEGVYRIGDQMDKQHDGMMRCTCVNGRGEMWTCIAYSQLRDQCIYDDITTYVNDT 530
| | | | |
QY 242 FHKRHEGHMLNCTCFGQGRGKRCDPVDOCSESTGFYQIGDSWEKYHGVRYOCYCY 301
| | | | |
Db 531 FHKRHEGHMLNCTCFGQGRGKRCDPVDOCSESTGFYQIGDSWEKYHGVRYOCYCY 590
| | | | |
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFIETPSPQNSHPIDW 341
| | | | |
Db 591 GRGIGEMHCOPLOTYPSSSGPVEVFIETPSPQNSHPIDW 630
| | | | |

RESULT 4
5455158-1
; Patent No. 5455158
; APPLICANT: VOGEL, TIKVA, LEVANON, AVIGDOR, WEBER, MOSHE M.;
; GUY, RACHEL, PANET, AMOS
; TITLE OF INVENTION: FIBRIN BINDING DOMAIN POLYPEPTIDES AND
; USES AND METHODS OF PRODUCING SAME
; NUMBER OF SEQUENCES: 20
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/58,241
; FILING DATE: 04-MAY-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 526,397
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: 345,952
; FILING DATE: 28-APR-1989
; APPLICATION NUMBER: 291,951
; FILING DATE: 29-DEC-1988
; SEQ ID NO: 1:
; LENGTH: 2327
5455158-1

Query Match 98.6%; Score 1973; DB 6; Length 2327;
Best Local Similarity 99.1%; Pred. No. 3.3e-174;
Matches 337; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAYYQOPHPQPPYGHCVTDSGVVSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
| | | | |
Db 263 AAYYQOPHPQPPYGHCVTDSGVVSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVTQT 322
| | | | |
QY 62 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSTSNYEODOKYSECTDHTVLVOT 121
| | | | |
Db 323 YGNSLNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSTSNYEODOKYSECTDHTVLVOT 382
| | | | |
QY 122 RGSNSGALCHFPFLYNNHNYTDCSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 181
| | | | |
Db 383 OGNSNGALCHFPFLYNNHNYTDCSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 442
| | | | |
QY 182 TTNEGVYRIGDQMDKQHDGMMRCTCVNGRGEMWTCIAYSQLRDQCIYDDITTYVNDT 241
| | | | |
Db 443 TTNEGVYRIGDQMDKQHDGMMRCTCVNGRGEMWTCIAYSQLRDQCIYDDITTYVNDT 502
| | | | |
QY 242 FHKRHEGHMLNCTCFGQGRGKRCDPVDOCSESTGFYQIGDSWEKYHGVRYOCYCY 301
| | | | |
Db 503 FHKRHEGHMLNCTCFGQGRGKRCDPVDOCSESTGFYQIGDSWEKYHGVRYOCYCY 562
| | | | |
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFIETPSPQNSHPIDW 341
| | | | |
Db 563 GRGIGEMHCOPLOTYPSSSGPVEVFIETPSPQNSHPIDW 602
| | | | |

RESULT 5
US-08-283-857-1
; Sequence 1, Application US/08283857
; Patent No. 5792742
; GENERAL INFORMATION:
; APPLICANT: GOLD, Leslie I.
; APPLICANT: ROSTAGNO, Agueda A.
; APPLICANT: BARON, Martin
; APPLICANT: CAMPBELL, Iain D.
; APPLICANT: WILLIAMS, Michael, J.
; TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
; TITLE OF INVENTION: CODING THEREFOR AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,857
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/714,134
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GOLD=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-283-857-1

Query Match 98.5%; Score 1971; DB 1; Length 2324;
Best Local Similarity 99.1%; Pred. No. 5e-174;
Matches 337; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAYYQOPHPQPPYGHCVTDSGVVSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVTQT 61
| | | | |
Db 260 AAYYQOPHPQPPYGHCVTDSGVVSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVTQT 319
| | | | |
QY 62 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSTSNYEODOKYSECTDHTVLVOT 121
| | | | |
Db 320 YGNSLNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCTSTSNYEODOKYSECTDHTVLVOT 379
| | | | |
QY 122 RGSNSGALCHFPFLYNNHNYTDCSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 181
| | | | |
Db 380 OGNSNGALCHFPFLYNNHNYTDCSEGRDNNKCGTTONYADOKFGFCPMAAHEIC 439
| | | | |
QY 182 TTNEGVYRIGDQMDKQHDGMMRCTCVNGRGEMWTCIAYSQLRDQCIYDDITTYVNDT 241
| | | | |
Db 440 TTNEGVYRIGDQMDKQHDGMMRCTCVNGRGEMWTCIAYSQLRDQCIYDDITTYVNDT 499
| | | | |
QY 242 FHKRHEGHMLNCTCFGQGRGKRCDPVDOCSESTGFYQIGDSWEKYHGVRYOCYCY 301
| | | | |
Db 500 FHKRHEGHMLNCTCFGQGRGKRCDPVDOCSESTGFYQIGDSWEKYHGVRYOCYCY 559
| | | | |
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFIETPSPQNSHPIDW 341
| | | | |

Db 560 GRGIGEMHCOPLOYYPSSSGPEVEFTTETPSQPNSHPIOW 599

RESULT 6

PCT-US95-09819-1
Sequence 1, Application PC/TUS9509819

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA

TITLE OF INVENTION: CODING THEREFOR AND USES THEREOF

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30 (EFO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09819

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/283,857

FILING DATE: 01-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: GOLD-1A PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-377-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2324 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-09819-1

Query Match 98.5%; Score 1971; DB 5; Length 2324;
Best Local Similarity 99.1%; Pred. No. 5e-174;
Matches 337; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

2 AAVYQPPHQPPEYGHCVTDGVSIVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
260 AAVYQPPHQPPEYGHCVTDGVSIVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 319
62 YGNSNGEPCVLPPTYNGRTFYSCCTEGRODGHLMCSYTSYEDOKXSFCTDHTVLVQT 121
320 YGNSNGEPCVLPPTYNGRTFYSCCTEGRODGHLMCSYTSYEDOKXSFCTDHTVLVQT 379
122 RGSNSNGALCHFPFLYNNHNTDCTSEGRNRMKCGTTOYVADOKRGFPMAAHEIC 181
380 QGGSNSNGALCHFPFLYNNHNTDCTSEGRNRMKCGTTOYVADOKRGFPMAAHEIC 439
182 TTNSGVNVRIGDDMDKDHMMRCCTVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 241
440 TTNSGVNVRIGDDMDKDHMMRCCTVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 499
242 FHKHEBGMHMLNCTCFQGRGRWKCDPYDQCDSETGTFYQIGDSWEKYVHGVYQCYCY 301
500 FHKHEBGMHMLNCTCFQGRGRWKCDPYDQCDSETGTFYQIGDSWEKYVHGVYQCYCY 559
302 GRGIGEMHCOPLOYYPSSSGPEVEFTTETPSQPNSHPIOW 341

Db 560 GRGIGEMHCOPLOYYPSSSGPEVEFTTETPSQPNSHPIOW 599

RESULT 7

US-08-153-799-16

Sequence 16, Application US/08153799

Patent No. 5766883

GENERAL INFORMATION:

APPLICANT: Ballance, David J

APPLICANT: Goodey, Andrew R

TITLE OF INVENTION: Polypeptides

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESSES:

ADDRESSEE: R Hain Swope, BOC Health Care Inc

STREET: 100 Mountain Avenue

CITY: Murray Hill

STATE: New Jersey

COUNTRY: USA

ZIP: 07974

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,799

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/847975

FILING DATE: 06-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8909916.2

FILING DATE: 29-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB90/00650

FILING DATE: 26-APR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/775952

FILING DATE: 29-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Swope, R Hain

REGISTRATION NUMBER: 24864

REFERENCE/DOCKET NUMBER: 92H832

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 665 2400

TELEFAX: (908) 771 6159

TELEX: 219484

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 2231 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: Protein

LOCATION: 1..2231

OTHER INFORMATION: /note= "Human fibronectin"

US-08-153-799-16

Query Match 97.9%; Score 1959; DB 1; Length 2231;
Best Local Similarity 99.1%; Pred. No. 6.2e-173;
Matches 336; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

2 AAVYQPPHQPPEYGHCVTDGVSIVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 61
260 AAVYQPPHQPPEYGHCVTDGVSIVGMQMLKTQGNKMLCTCLGNGVSCQETAVTQT 319
62 YGNSNGEPCVLPPTYNGRTFYSCCTEGRODGHLMCSYTSYEDOKXSFCTDHTVLVQT 121

Db 320 YGNSNGEPCVLPFTYNGRTFYSCTEGRODGLMCSSTSNBYODOKYSFCTDHTLVOT 379
QY 122 RGNNGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADOKFGFCMAAHEBIC 181
Db 380 QGNSNGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADOKFGFCMAAHEBIC 439
QY 182 TTNEGVMYRIGDOWDKOHDMGMMRCTCVNGRGWTCIAVSQLRDQCIYDITVNVNDT 241
Db 440 TTNEGVMYRIGDOWDKOHDMGMMRCTCVNGRGWTCIAVSQLRDQCIYDITVNVNDT 499
QY 242 FKRHEGMMNLCTCGQGGGRMKCDPVDCODSEGTGTQIDSWEKYVGVRYOCYCY 301
Db 500 FKRHEGMMNLCTCGQGGGRMKCDPVDCODSEGTGTQIDSWEKYVGVRYOCYCY 559
QY 302 GRGIGWHCOPLOTYPSSSGPVEFTTTPSPNSHPIQ 340
Db 560 GRGIGWHCOPLOTYPSSSGPVEFTTTPSPNSHPIQ 598

RESULT 8

US-08-448-489-17
Sequence 17, Application US/08448489
Patent No. 6184022
GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 631
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Known Member of
US-08-448-489-17

Query Match 19.1%; Score 382.5; DB 3; Length 631;
Best Local Similarity 38.3%; Pred. No. 2.9e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;
QY 55 ETAVTQTYGNSNGEPCVLPFTYNGRTFYSCTEGRODGLMCSSTSNBYODOKYSFCTD 114
Db 188 EGQVAVVKYGNADGEYCKPFFLFNGKEKYNSTCTDGRSDGFLMCSSTYNEFKDGKYGFC-P 246
QY 115 HTVLVOTRGNSNGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADOKFGFCPM 174
Db 247 HEALF-TMGNAAGOPCKPFRFGTSTYSCCTEGRTDGRWCGTTEDYDRDKYGCPE 305
QY 175 AAHEBICITNEGV-----MYRIGDOWDKOHDMGMMRCTCVNGRGWTCIA---YSQLR 226
Db 306 TASTYVGNSEGAFCVFPFTFLGNKYES-----CTSAGSDGKMKCATYANVDDDR 356
QY 227 DQCIYDITVNVNDTFRKHEBGMHL 252
Db 357 KMGFCPDQGYSL--FLVAHEFGHAM 380

RESULT 9
US-08-704-711A-18
Sequence 18, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
NUMBER OF SEQUENCES: 22
METALLOPROTEASES, THEIR PRODUCTION AND USE

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-18

Query Match 19.1%; Score 382.5; DB 3; Length 660;
Best Local Similarity 38.3%; Pred. No. 3e-27;
Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;
QY 55 ETAVTQTYGNSNGEPCVLPFTYNGRTFYSCTEGRODGLMCSSTSNBYODOKYSFCTD 114
Db 217 EGQVAVVKYGNADGEYCKPFFLFNGKEKYNSTCTDGRSDGFLMCSSTYNEFKDGKYGFC-P 275
QY 115 HTVLVOTRGNSNGALCHPEFLYNNHNYTDCSEGRDNMKCGTTONYADOKFGFCPM 174
Db 276 HEALF-TMGNAAGOPCKPFRFGTSTYSCCTEGRTDGRWCGTTEDYDRDKYGCPE 334
QY 175 AAHEBICITNEGV-----MYRIGDOWDKOHDMGMMRCTCVNGRGWTCIA---YSQLR 226
Db 335 TASTYVGNSEGAFCVFPFTFLGNKYES-----CTSAGSDGKMKCATYANVDDDR 385
QY 227 DQCIYDITVNVNDTFRKHEBGMHL 252
Db 386 KMGFCPDQGYSL--FLVAHEFGHAM 409

RESULT 10
US-09-521-220-18
Sequence 18, Application US/09521220
Patent No. 6393348
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
NUMBER OF SEQUENCES: 22
METALLOPROTEASES, THEIR PRODUCTION AND USE
CORRESPONDENCE ADDRESS:

QY 175 AAHEICTNEGV-----MYRIGDQMDKOHDMGMNRCCTCVGNGSGEWTCTIAYSQLRDO- 228
DB 332 TAWSTVGNSSEGAFCVFPFIFLGNTYDS-----CTSGANDGKLMCASTSYSDDDR 382
QY 229 ----CIVDDITVYVNDTFKRRHEGML 252
DB 383 KMGFC--PDQGYSL--FLVAAHBFHAM 406

RESULT 13

US-09-194-468A-45
Sequence 45, Application US/09194468A
Patent No. 6500924
GENERAL INFORMATION:
APPLICANT: Brooks, Peter
APPLICANT: Cheresch, David A
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
FILE REFERENCE: MER00495
CURRENT FILING DATE: 1999-03-23
PRIOR FILING DATE: 1996-05-31
PRIOR FILING DATE: 1996-05-31
PRIOR FILING DATE: 1996-05-31
PRIOR FILING DATE: 1996-05-31
PRIOR FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 429
TYPE: PRT
ORGANISM: Homo sapiens
US-09-194-468A-45

Query Match 19.0%; Score 380; DB 4; Length 429;
Best Local Similarity 45.0%; Pred. No. 3e-27;
Matches 77; Conservative 20; Mismatches 56; Indels 18; Gaps 6;

QY 16 YGHCVTDSGVVYSVGMQMLKTQGNKOMLCTCLANGVSCQETAVTYQYGGNSNEPCVLPF 75
DB 13 YNSC-TDTG--RSDGFLMCTTYNFEK---DKYGFCEPHEALF-TWGGNAECPCKFPF 64
QY 76 TNGRFTVYSCCTEGRDGHLWCSTTSNYEODKYSFCTHTVLYQVRGNSNALCH 135
DB 65 RFGGTSYDSTCTTGRTDGYWCGTTEYDCKYGFCEP--TAWSTVGNSSEGAFCVFPF 122
QY 136 LVNNHNYTDCSTSEGRDNMKCGTTONYADOKFGFCP-----MAAHE 178
DB 123 TFLGNKYESTSGRSGDKMKWCATTANYDDRKMGFCPDQGYSLFLVAAHE 173

RESULT 14

US-08-704-711A-19
Sequence 19, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 707 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-19

Query Match 18.7%; Score 374; DB 3; Length 707;
Best Local Similarity 40.1%; Pred. No. 2e-26;
Matches 77; Conservative 29; Mismatches 56; Indels 30; Gaps 7;

QY 16 YGHCVTDSGVVYSVGMQMLKTQGNKOMLCTCLANGVSCQETAVTYQYGGNSNEPCVLPF 75
DB 241 YSACTTDDG--ISDGLPWCSTTANYD---TDRFRCPSERLYTR--DGNADGKPCQFPF 292
QY 76 TNGRFTVYSCCTEGRDGHLWCSTTSNYEODKYSFCTHTVLYQVRGNSNALCH 132
DB 293 IFQGGYSYACTTGRDGRWCATTANYDRDKUFGCPTRADSTV-----GGSABLCV 348
QY 133 FPLVNNHNYTDCSTSEGRDNMKCGTTONYADOKFGFCP-----MAAHE----- 178
DB 349 FPFRTFKYKYSTSTSGRDRGRLWCATTISNFDKDKMGFCPDQGYSLFLVAAHFGHALG 408
QY 179 -EICTNEGVY 189
DB 409 LDHSSVPEALMY 420

RESULT 15

US-09-521-220-19
Sequence 19, Application US/09521220
Patent No. 6399348
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/521,220

FILING DATE: 08-Mar-2000

CLASSIFICATION: <Unknown>
21-OCT-1994

21-OCT-1994
17-MAR-1994

17-MAR-1994

APPLICATION NUMBER: 08/704,711

FILING DATE: <Unknown>

APPLICATION NUMBER: DE

FILING DATE: 21-OCT-1994

APPLICATION NUMBER: DE 4409663.1

FILING DATE: 17-MAR-1994

AGENCY/AGENT INFORMATION:

NAME: GRANADOS, Patricia D.

REGISTRATION NUMBER: 33,683

REFERENCE/DOCKET NUMBER: 26083/1124

TELEPHONE: (202) 672-5300

TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

TELEFAX: (202) 612-3399
TELEX: 904136

ADDED: 201100
ON FOR SEQ ID NO: 19:

CHARACTERISTICS:

LENGTH: 707 amino ac

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

ENCE DESCRIPTION: SEQ

6T-

Match 18-7%: Score 374:

Local Sim

Query Match	18.7%;	Score 374;	DB 4;	Length 707;
Best Local Similarity	40.1%;	Pred. No. 2e-26;		
Matches 77;	Conservative 29;	Mismatches 56;	Indels 30;	Gaps 7;

THE UNIVERSITY OF CHICAGO

16 YGHCVTDSGVVYSVGMQWLKTQGNKQMLCTCLGNVSCQETA VTQTYYGNSNGEPCVLPF 75

0y 16 YGHCTDSDGVVYVSGMQLKTKGNKCOMLCTCLSGNVSGQETAVNQTGGNSNGEPCVLPBF 75
 241 VSLGMMDD - - - - - DEDCT DWGCGMAYVN - - - - - TTTTGGCGGCGGATTTT VMD - - - - - DQITDCTGTCGCTT 200

DB 241 YSACTIDG---KSDGLPWCSTIANYD---IDDKFGFCPSERLYIR--DGNADGKPCQPPF 292

OV 76 TYNGRTFYSCCTTEGRDGLWCSTTSNYEODOKYSEC--TDHTVI.VOTRGGNSNGAI.CH 132

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 104

Db 293 IFQGQSYSACTTDGRSDGYRWCATTANYDRDKLFGFCPTRADSTM---GGNSAGELCV 348

[illegible]

QY 133 PPFLYNNHNYTDCTSEGRDNMKWCGTTQNYDADQKFGFCP-----MAAHE----- 178

[illegible]

Db 349 FPFLEKEYSTICTSEGRGDGRWCATTSNFSDDKKWGFCPDQGYSLFLVAAHEFGHALG 408

0V 179 -ETCTNEGVMY 189

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:11 / Search time 42 Seconds
(without alignments)
2107.430 Million cell updates/sec

Title: US-09-934-706-1

Perfect score: 2002

Sequence: 1 MAAYVQPPHQPYPYGHCV.....EVEFTTPSQNSHPICWLE 343

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1988	99.3	657	4	Q81V18
2	1422	71.0	922	13	Q93405
3	1422	71.0	2478	13	Q93406
4	1190	59.4	205	4	Q9HAP3
5	1091	54.5	379	4	Q95610
6	750	37.5	141	13	Q90XQ2
7	405	20.2	679	13	Q98856
8	392	19.6	675	13	Q98856
9	391	19.5	690	13	Q98856
10	389.5	19.5	671	13	Q98856
11	383.5	19.2	655	13	Q98856
12	383.5	19.2	673	13	Q98856
13	381.5	19.1	632	13	Q98856
14	379.5	19.0	686	13	Q98856
15	378.5	18.9	661	6	Q95J74
16	378	18.9	707	4	Q8N725

17	377.5	18.9	674	13	Q98TC6	Q98TC6 cyprinus ca
18	374.5	18.7	385	6	Q9TUL8	Q9TUL8 equus caball
19	372.5	18.6	661	6	Q9GLE5	Q9GLE5 bos taurus
20	366	18.3	704	6	Q19130	Q19130 canis famill
21	365.5	18.3	657	13	Q9PTU7	Q9PTU7 oxyzias lat
22	360	18.0	656	13	Q8BUZ3	Q8BUZ3 xenopus lae
23	359.5	18.0	658	13	Q90YB4	Q90YB4 parailichthy
24	348	17.4	296	11	Q8C6J7	Q8C6J7 mus musculu
25	326	16.3	208	6	Q9XSD1	Q9XSD1 canis famill
26	317	15.8	324	6	Q9N282	Q9N282 bos taurus
27	316.5	15.8	111	6	Q95166	Q95166 canis famill
28	272.5	13.6	223	4	Q96RT0	Q96RT0 mus musculu
29	269.5	13.5	220	4	Q9H4C8	Q9H4C8 mus musculu
30	269.5	13.5	223	4	Q96H33	Q96H33 mus musculu
31	261	13.0	245	6	Q9GJ25	Q9GJ25 canis famill
32	261	13.0	261	6	Q9GJ26	Q9GJ26 canis famill
33	242.5	12.1	638	13	Q8AX63	Q8AX63 silurus aso
34	232.5	11.6	216	11	Q99XDO	Q99XDO mus musculu
35	232.5	11.6	810	11	Q8R3F3	Q8R3F3 mus musculu
36	217	10.8	351	6	Q02816	Q02816 oryctolagus
37	214	10.7	153	4	Q9H382	Q9H382 mus musculu
38	203	10.1	1326	4	Q13019	Q13019 mus musculu
39	203	10.1	1465	4	Q13018	Q13018 mus musculu
40	202	10.1	320	4	Q96KP8	Q96KP8 mus musculu
41	202	10.1	1456	11	Q61830	Q61830 mus musculu
42	199.5	10.0	320	6	Q95KV4	Q95KV4 bos taurus
43	195	9.7	653	11	Q8VCS4	Q8VCS4 mus musculu
44	194	9.7	2328	6	Q95MT9	Q95MT9 etineaceus e
45	193.5	9.7	1479	4	Q9Y5P9	Q9Y5P9 mus musculu

ALIGNMENTS

RESULT 1	ID	Q81V18	PRELIMINARY;	PRT;	657 AA.
AC	Q81V18				
DT	01-MAR-2003 (TREMURel. 23, Created)				
DT	01-MAR-2003 (TREMURel. 23, Last sequence update)				
DT	01-MAR-2003 (TREMURel. 23, Last annotation update)				
DE	Migration stimulation factor FN70+.				
GN	FN.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Schor S.L., Schor A.M., Kay R.A.;				
RT	"The sequence of MSF/FN70 + variant."				
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AJ535086; CAD59389.1; -				
SQ	SEQUENCE 657 AA; 73752 MW; 8CA04E64486ABCD0 CRC64;				

Query Match	Best Local Similarity	99.3%;	Score 1988;	DB 4;	Length 657;
Matches	340;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
QY	2	AAAYVQPPHQPYPYGHCVTDGVSVMQWKTQGNKQMLCTCLGNGVSCQETAVTOR	61		
DB	291	AAAYVQPPHQPYPYGHCVTDGVSVMQWKTQGNKQMLCTCLGNGVSCQETAVTOR	350		
QY	62	YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSITSNYBQDKYSECTDHTLVQ	121		
DB	351	YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSITSNYBQDKYSECTDHTLVQ	410		
QY	122	RGNSNGALCHPFLVNNHNYTCTSEGRDNNKNGCTTQNTADOKFGCPAAAEETC	181		
DB	411	RGNSNGALCHPFLVNNHNYTCTSEGRDNNKNGCTTQNTADOKFGCPAAAEETC	470		
QY	182	TTTEGVVYRIGDQWDQKHDMGHHMRCICVNGNGEWTCTAYSQLROCCIYDDITVW	241		

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Db 471 TTNEGVWYRIDQWDKQHDHMHMECTCVNGRGWTCIAYSQLRDQCIYDDITVNVNDT 530
QY 242 FHKHHEGHMLNCTCFQGGGRWKCDPYDQOCDSSETGTFYQIGDSWEKYVHGVRYQCYC 301
Db 531 FHKHHEGHMLNCTCFQGGGRWKCDPYDQOCDSSETGTFYQIGDSWEKYVHGVRYQCYC 590
QY 302 GRGIGEMWCPLOTYPSSSGPVEVFITETPSQPNSHPIQW 341
Db 591 GRGIGEMWCPLOTYPSSSGPVEVFITETPSQPNSHPIQW 630

RESULT 2
ID 093405 PRELIMINARY; PRT; 922 AA.
AC 093405;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Fibronectin.
GN FN1 OR FN2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao O., Collodi P.;
RT "Characterization and expression of zebrafish fibronectin.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081127; AAC31941.1; -.
DR HSSP; P02751; 1FBR.
DR ZFIN; ZDB-GENE-000426-1; fn1.
DR InterPro; IPR000083; Fibnrcn1.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR00562; FN_Type_II.
DR Pfam; PF00039; fn1; 9.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00013; FNTYPEII.
DR PRODOM; PD00095; FN_Type_II; 2.
DR SMART; SM00058; FN1; 9.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01253; FIBRONECTIN_1; 9.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
SQ SEQUENCE 922 AA; 101814 MW; EF83E4CACBD0080 CRC64;

Query Match 71.0%; Score 1422; DB 13; Length 922;
Best Local Similarity 68.6%; Pred. No. 1e-125;
Matches 234; Conservative 48; Mismatches 57; Indels 2; Gaps 2;
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Db 587 YGNIGELSCPEHISGHRPVQVITSEAGNPNSHPIQW 627
Db 587 YGNIGELSCPEHISGHRPVQVITSEAGNPNSHPIQW 627

RESULT 3
ID 093406 PRELIMINARY; PRT; 2478 AA.
AC 093406;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Fibronectin.
GN FN1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao O., Collodi P.;
RT "Characterization and expression of zebrafish fibronectin.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081128; AAC31947.1; -.
DR HSSP; P02751; 1FBR.
DR ZFIN; ZDB-GENE-000426-1; fn1.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR000083; Fibnrcn1.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR00562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRODOM; PD00095; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 14.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 11.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
SQ SEQUENCE 2478 AA; 271652 MW; A03475C5A8385750 CRC64;

Query Match 71.0%; Score 1422; DB 13; Length 2478;
Best Local Similarity 68.6%; Pred. No. 3.3e-125;
Matches 234; Conservative 48; Mismatches 57; Indels 2; Gaps 2;
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ID 09HAP3 PRELIMINARY; PRT; 205 AA.
AC 09HAP3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Fibronection (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN 1[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=55284965; PubMed=2992939;
RA Kornblith A.R., Umezawa K., Vide-Pedersen K., Baralle F.E.;
RT "Primary structure of human fibronection: differential splicing may
RT generate at least 10 polypeptides from a single gene.";
RL EMBL J. 4:175-179 (1985).
RN 1[2]
RP SEQUENCE FROM N.A.
RA Steffensen B., Martin P.A.;
RT "Fibronection collagen binding domain (modules I6, I11, I12, I17).";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF312399; AAG30571.1; -.
DR HSSP; P02751; 2FN2.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 2.
DR Pfam; PF00040; fn2; 2.
DR PRINTS; PR00012; FNTYPEII.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 2.
DR SMART; SM00059; FN2; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 2.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
FT NON_TER 1 50 S -> L (IN REF. 1).
FT CONFLICT 106 106 R -> Q (IN REF. 1).
FT NON_TER 205 205
SQ SEQUENCE 205 AA; 22947 MW; B423205B9B65F989 CRC64;

Query Match 59.4%; Score 1190; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GHCVTDSGVVSYGVGMQLTKQGNKQMLCTCLGNGVSCQETAVTQTGNSNGEPCVLPFT 76
DB 1 GHCVTDSGVVSYGVGMQLTKQGNKQMLCTCLGNGVSCQETAVTQTGNSNGEPCVLPFT 60
QY 77 YNRTFPTSCCTBERODGHLWCSTTSNEDQOKYSFCTDHTVLVQTRGNSNGALCHPPEL 136
DB 61 YNRTFPTSCCTBERODGHLWCSTTSNEDQOKYSFCTDHTVLVQTRGNSNGALCHPPEL 120
QY 137 YNNHNTYDCTSEGRPRDMMKMGCTTQNYADADQKFGFCPMAAHEICTTNEGVMYRIGDQMD 196
DB 121 YNNHNTYDCTSEGRPRDMMKMGCTTQNYADADQKFGFCPMAAHEICTTNEGVMYRIGDQMD 180
QY 197 KQHDGMGMNRCCTCVNGRGEMWTCA 221
DB 181 KQHDGMGMNRCCTCVNGRGEMWTCA 205

RESULT 5
095610 PRELIMINARY; PRT; 379 AA.
AC 095610;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fibronection (Fragment).
FN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN 1[1]
RP SEQUENCE FROM N.A.
RA Godfrey H.P., Ebrahim A.A.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U42404; AAD00015.1; -.
DR HSSP; P02751; 1FBR.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 6.
DR Pfam; PF00040; fn2; 2.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 5.
DR SMART; SM00059; FN2; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 4.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
FT NON_TER 1 379
FT NON_TER 379 379
SQ SEQUENCE 379 AA; 42191 MW; 319FF9C844059542 CRC64;

Query Match 54.5%; Score 1091; DB 4; Length 379;
Best Local Similarity 99.0%; Pred. No. 6.9e-95;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAYQOPHPQPPYGHCVTDSGVVSYGVGMQLTKQGNKQMLCTCLGNGVSCQETAVTQT 61
DB 189 AAYQOPHPQPPYGHCVTDSGVVSYGVGMQLTKQGNKQMLCTCLGNGVSCQETAVTQT 248
QY 62 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNEDQOKYSFCTDHTVLVQT 121
DB 249 YGNSNGEPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNEDQOKYSFCTDHTVLVQT 308
QY 122 RGSNSGALCHPPELYNNHNTYDCTSEGRPRDMMKMGCTTQNYADADQKFGFCPMAAHEIC 181
DB 309 RGSNSGALCHPPELYNNHNTYDCTSEGRPRDMMKMGCTTQNYADADQKFGFCPMAAHEIC 368
QY 182 TTNEGVMYRIG 192
DB 369 TTNEGVMYRIG 379

RESULT 6
090X02 PRELIMINARY; PRT; 141 AA.
AC 090X02;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fibronection (Fragment).
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxId=8296;
RN 1[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21439472; PubMed=11555861;
RA Christensen R.N., Weinstein M., Taassava R.A.;
RT "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
RT and semi-quantitative RT-PCR expression studies.";
RL J. Exp. Zool. 290:529-540 (2001).
DR EMBL; AF360987; AAL16960.1; -.
DR InterPro; IPR000083; Fibrnctnl.
DR Pfam; PF00039; fn1; 3.
DR PRINTS; PR00012; FNTYPEII.
DR SMART; SM00058; FN1; 3.
DR PROSITE; PS01253; FIBRONECTIN_1; 2.
FT NON_TER 1 141
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 16571 MW; F5E7443B27D2593C CRC64;

Query Match 37.5%; Score 750; DB 13; Length 141;
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Best Local Similarity 87.9%; Pred. No. 3.7e-63;
Matches 124; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 169 FGFCPMAAHEICTTNEGVMFRIGDQMDKDHMMKCTCVGNGRGEMTCIAVSQSLDQ 228
Db 1 FGFCPMAAHEICTTNEGVMFRIGDQMDKDHMMKCTCVGNGRGEMTCIAVSQSLDQ 60
QY 229 CIVDDITYNVNDTFHKRHEBGMHMLNCTCFGGGRGKCDPVDQCODSETGTFTYQIGDSWE 288
Db 61 CIVDDITYNVNDTFHKRHEBGMHMLNCTCFGGGRGKCDPVDQCODSETGTFTYQIGDSWE 120
QY 289 KYVHGVRVQCYCGRGIGEMH 309
Db 121 KYVHGVRVQCYCGRGIGEMH 141

RESULT 7

QY 098856 PRELIMINARY; PRT; 679 AA.
AC Q98856, TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Gelatinase-b.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=96270627; PubMed=8692902;
RA Miyazaki K., Uchiyama K., Imokawa Y., Yoshizato K.;
RT "Cloning and characterization of cDNAs for matrix metalloproteinases
RT of regenerating new limbs."
RL Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824(1996).
DR EMBL; D82052; BA01523.1; -.
DR HSSP; P02751; 2FN2.
DR MEROPS; M10.004; -.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrxin.
DR InterPro; IPR006026; Zn_MTPeptidase.
DR InterPro; IPR006025; Zn_MTPeptidase.
DR Pfam; PF00040; fn2_3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; peptidase_M10_N; 1.
DR Pfam; PF03933; peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00013; MATRXIN.
DR ProDom; PD000955; FN_Type_II; 3.
DR SMART; SM00059; FN2_3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 679 AA; 75581 MW; 573CDB9DBF85524 CRC64;

Query Match 20.2%; Score 405; DB 13; Length 679;

Best Local Similarity 30.2%; Pred. No. 1e-29;
Matches 98; Conservative 39; Mismatches 88; Indels 100; Gaps 12;

QY 47 LGNVSOCEATVATQTYGNSNGEPCVLPFTYNGRTFTYCTTEGRDGLMSTTSNVED 106
Db 213 LGTV-----VTKRFENANGAACKEPFKNGNSYSTSEGRDGLMSTTTDDXD 266
QY 107 QKYSFCTDHTVLVQTRGNSNGALCHPPLFLNNHNYTCTSEGRDNNKMGCTTQNYDAD 166
Db 267 KKYVFCFCE--LTYTGNSDGDCKVFFPIDGSDYDCTEGSDGGRMCAITDNPFD 324
QY 167 QKGFCEPMAAHEICTTNEGVMFRIGDQMDKDHMMKCTCVGNGRGEMTCIAVSQ 224

Db 325 KKYVFCP-----:|||||-----| | | | | :|
QY 225 LRDDCIVDDITYNVNDTFHKRHEBGMHMLNCTCFGGGRGKCDPVDQ-----CQDS 275
Db 345 --DPCVPPFP--LEKTYH-----SCTSDGRGRKIMCATTSSYSDRKKGFPPDQ 391

QY 276 ETGTF-----YQIGDS-----MEKYHGVRYQ-----CYCGRGIGEMH 309
Db 392 GYSLFLVGAHGFHAIQLHSTYDALMPMFRIEFGQLHDDIEGVQLYLGSQTGPHR 451
QY 310 CQPLQT--YPSGQVGFITETPS 332
Db 452 SPMPTTKSPDVSGKTTTVTTSPT 476

RESULT 8

QY 080F06 PRELIMINARY; PRT; 675 AA.
AC Q80F06, TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Matrix metalloproteinase 9 precursor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson M.C.M., Sangrador-Vegas A., Smith T.J.;
RT "Cloning and characterisation of the rainbow trout (Oncorhynchus
RT mykiss) mmp9 mRNA."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ320533; CAC85923.1; -.
DR HSSP; P39900; L01Z.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrxin.
DR InterPro; IPR006026; Zn_MTPeptidase.
DR InterPro; IPR006025; Zn_MTPeptidase.
DR Pfam; PF00040; fn2_3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; peptidase_M10_N; 1.
DR Pfam; PF03933; peptidase_M10_N; 1.
DR ProDom; PD000955; FN_Type_II; 3.
DR SMART; SM00059; FN2_3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR HydroLase; Metal-binding; Metalloprotease; Protease; Signal; Zinc.
FT SIGNAL 1 19
SQ SEQUENCE 675 AA; 75261 MW; 84A78BD96DB569E CRC64;

Query Match 19.6%; Score 392; DB 13; Length 675;

Best Local Similarity 27.8%; Pred. No. 1.7e-28;
Matches 105; Conservative 37; Mismatches 100; Indels 136; Gaps 14;

QY 10 HPQPPPG-----HCVTDSGVVSVGMQLKTQGNKO-MTC-----TCLNGV 51
Db 191 HAPFGGCIQGDHAFDDENWTLGKGAUVTSNGNAGALCHPFPFGKQYSTCTTEGR 250
QY 52 S-----CQETA-----VTQTYGNSNGEPCVLPFTYNGRTFTYCTTEGRD 92
Db 251 SDNLPMCATTAADGRDKKFCSELLYTFDGNNGKACVFPFVLGETYEGCTTEGRSD 310
QY 93 GHLWCSTTSNVEDQKSFCTDHTVLVQTRGNSNGALCHPPLFLNNHNYTCTSEGRD 152
Db 311 GYRWCSTTENFDKDKKGFQPNBDTAV--TGNSEBGPCHFPVFLGNKYDSCSTSEGRD 368

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QY 153 NMKCGTTONYADADOKFECF-----MAAHEICTTNEGVMYRIGDQWDRKHDMGHM 204
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 GRMCMATTSNFDYDTKMGFCQDGRGYSFLVAAHE-----FGHA 406
QY 205 MRCTCVNGRGEWTCIAYSQLRQDCIVDDITVNVNDTFHRRHEGHMLNCTCGGGRGEM 264
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 407 LG-----LDHNRNALMVMYMSYVEDFSLKHDDVEG----- 438
QY 265 KCDPVQCQDSERTGTVOIGDSWEKYGVRQCYCGRGIGMHCQPLQTYSSSGP-- 322
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 439 -----IH-----YLYGSKTGP--DPIPTIP-SGPPDP 462
QY 323 -VEVFITETPSQNSHPI 339
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 463 KPDITTKSTTTTTHPV 480

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RESULT 9

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ID 09PVMS PRELIMINARY; PRT; 690 AA.
AC 09PVMS;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Gelatinase B.
GN GEL-B.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20363695; PubMed=10903498;
  Matsui H., Ogiwara K., Onkura R., Yamashita M., Takahashi T.;
  "Expression of gelatinases A and B in the ovary of the medaka fish
  RT Oryzias latipes";
  Eur. J. Biochem. 267:4658-4668 (2000).
DR EMBL; AB033755; BAA85770.1; -.
DR HSSP; P08254; IHFS.
DR MEROPS; M10.004; -.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR006026; Nzn_MTPeptidase.
DR InterPro; IPR006025; Zn_MTPeptidase.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; ENTYPBET.
DR PRINTS; PR00138; MATRXIN.
DR PRODOM; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HK; 4.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolyase; Metal-binding; Metalloprotease; Protease; Zinc.
SQ SEQUENCE 690 AA; 77610 MW; 43507186ED9BD088 CRC64;

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Query Match 19.5%; Score 391; DB 13; Length 690;

Best Local Similarity 32.1%; Pred. No. 2,1e-28;

Matches 96; Conservative 41; Mismatches 116; Indels 46; Gaps 10;

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QY 47 LGNGVSCQETAVTGTGNSNGEPCVLPFTYNGRTFTSCCTEGRODGLMCTTSNYEOD 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 214 LGKG-----PVKTYVGNADGAMCHPFPVFGGKTYTSCISEGRADLPMWCSTDDYDRD 267

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QY 107 OKYSFCTDHTVLVOTRGNSNGALCHFPFLYNNHNYTDTSEGRBDNMKCGTTONYAD 166
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 268 GKXGFCPSR--LLYITIGNSDGAACVFPFVLGDEYDSCSTTSGRRRGYMCATTSYDOD 325
QY 167 QKRGFCPMAAHEICTTNEGVMYR-----IGDQWDRKHDMGHMRCCTCVNGRGE-W--T 218
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 326 KXYGFCPNTDTTITIGNAEGEPCHPFPFELGKEYDS-----CTSGRGDGGKLMCGT 376
QY 219 CIAYSQLRQDCIVDDITVNVNDTFHRRHEGHMLNCTCGGGRGKCDPVQCQDSERG 278
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 377 TASYDDKKMGKCPDQGISL--FLVAAHEFGHALG-----DHSNRDALMY 421
QY 279 TFYQIGDSW---EKYHGVRYQCYCGRGIGMHCQPLQTYSSSGPVEFITETPSOP 334
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 422 PMYSYVEDFSLHEDDLEGIQ---YLYGSKTDPKPTVPQKPPPTTATPPDPDVTSDTDEP 477

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RESULT 10

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ID 09W7L6 PRELIMINARY; PRT; 671 AA.
AC 09W7L6;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Gelatinase B.
GN MMP-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX "xmp-9 (Gelatinase B) is Expressed During Wound Healing,
  RT Regeneration, and Development.";
  Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072455; AAD41624.1; -.
DR HSSP; P08254; IUSN.
DR MEROPS; M10.004; -.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR006026; Nzn_MTPeptidase.
DR InterPro; IPR006025; Zn_MTPeptidase.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; ENTYPBET.
DR PRINTS; PR00138; MATRXIN.
DR PRODOM; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HK; 4.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolyase; Metal-binding; Metalloprotease; Protease; Zinc.
SQ SEQUENCE 671 AA; 74845 MW; 14D6A052D69FAFE CRC64;

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Query Match 19.5%; Score 389.5; DB 13; Length 671;

Best Local Similarity 45.1%; Pred. No. 2,9e-28;

Matches 74; Conservative 20; Mismatches 45; Indels 25; Gaps 4;

```

QY 28 SVGMOWLKT-----QGNKQMLCTCLANGVSCQETAVTGTGNSNGEPCVLPFTYNGRTF 82
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 SDGLPMWCSTTPNVDDKKYGF-----PSEKLYTIGNSNGQPCVLPFTYNGVSY 298
QY 83 YSCCTEGRODGLMCTTSNYEODOKYSFCTDHTVLVOTRGNSNGALCHFPFLYNNHNY 142
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 299 NGCTKEGRDGYRWKCSTTANFDQDKKYGFCPNRDTSV--IGNSQCEPCVFPFTFLGKIH 356

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Db 419 MYPMYTYVEDPFLAHKODIEGIVLYGKGTG-----PDPPTPPQPTSTTTTPN-PTG 467
 QY 337 HP 338
 Db 468 EP 469

RESULT 13
 ID 09N1P6 PRELIMINARY; PRT; 632 AA.
 AC 09N1P6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
 DE Matrix metalloproteinase-2 (Fragment).
 GN MMP-2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=fibrosarcoma;
 RA Jalic H., Paria B., Balkin R., Baxendale V., Fang Y., Kitchell B.,
 RT "Cloning of matrix metalloproteinase-2 (MMP-2) from canine
 fibrosarcoma.";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF177217; AAF67517.1; -
 DR HSSP; P08253; 1RTG.
 DR INTERPRO; IPR000562; FN_Type_II.
 DR INTERPRO; IPR000585; Hemopexin.
 DR INTERPRO; IPR001818; Matrixin.
 DR INTERPRO; IPR006026; Nzn_MTPeptide.
 DR INTERPRO; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; ENTPEPIL.
 DR PRINTS; PR00138; MATRIXIN.
 DR PRODOM; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KM Hydrolyase; Metal-binding; Metalloprotease; Protease; Zinc.
 FT NON_TER 1
 SQ SEQUENCE 632 AA; 70991 MW; D8AE895497E129F3 CRC64;

Query Match 19.1%; Score 381.5; DB 6; Length 632;
 Best Local Similarity 39.3%; Pred. No. 1.5e-21; Matches 81; Conservative 26; Mismatches 78; Indels 21; Gaps 6;

QY 55 ETAVTQTGGNSGECVLPFTYNGRTFVSCCTEGRDGHLWCSTSNYEDOKYSCFCTD 114
 Db 189 EGVVAVKVGNNADGEYCKPFLNGREYVSTCTDGRSDGLWCSTYTNFKDKYGC-P 247
 QY 115 HTVLVOTRGNSGALCHPFLNNHNYTDTCTSEGRDNMKKCGTTONTYADOKFGFCPM 174
 Db 248 HEALF-TMGNNADGQCKPFFRCGTSTYSDCTTEGRTDGYRWGCTEDYDRDKKYGFCPE 306
 QY 175 AAHEICTTNGV-----MYRIGDQMDKQDMGMKRCCTCVGNGRGEMTCTIA---VSQR 226
 Db 307 TASTTIGNSEGAPCVFPFTFLGKHS-----CTASGNSDGVKWCATTANYDDDR 357
 QY 227 DQCIIVDTITVNVDTFKHREEGHML 252
 Db 358 KMGFCPDGYSYSL--FLVAHAHFGHAM 381

RESULT 14
 ID 09DE15 PRELIMINARY; PRT; 686 AA.
 AC 09DE15;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
 DE 75 kDa gelatinase.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20576236; PubMed=11010969;
 RA Hahn-Dantona E.A., Ames R.T., Quigley J.P.;
 RT "The isolation, characterization, and molecular cloning of a 75-kDa
 gelatinase B-like enzyme, a member of the matrix metalloproteinase
 (MMP) family. An avian enzyme that is MMP-9-like in its cell
 expression pattern but diverges from mammalian gelatinase B in
 sequence and biochemical properties.";
 RL J. Biol. Chem. 275:40827-40838(2000).
 DR EMBL; AF222690; AAG47650.1; -
 DR HSSP; P08254; ISLM.
 DR INTERPRO; IPR000562; FN_Type_II.
 DR INTERPRO; IPR000585; Hemopexin.
 DR INTERPRO; IPR001818; Matrixin.
 DR INTERPRO; IPR006026; Nzn_MTPeptide.
 DR INTERPRO; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; ENTPEPIL.
 DR PRINTS; PR00138; MATRIXIN.
 DR PRODOM; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KM Hydrolyase; Metal-binding; Metalloprotease; Protease; Zinc.
 SQ SEQUENCE 686 AA; 76679 MW; 9E9AB59F6A497CE CRC64;

Query Match 19.0%; Score 379.5; DB 13; Length 686;
 Best Local Similarity 28.7%; Pred. No. 2.6e-27; Matches 99; Conservative 45; Mismatches 82; Indels 119; Gaps 15;

QY 16 YGHCVTDGVSIVSGNQLTKQGNKMLCT---CLNGVSCQETAVTQYVGSNSGPCV 72
 Db 241 YSKCITEG--RDGLMKCATTA SYADKTYGC-----PSLLYTNGSNSDGSPCV 289
 QY 73 LPFTYNGRTFVSCCTEGRDGHLWCSTSNYEDOKYSCFCTD- TVLVOTRGNSGALC 131
 Db 290 FPFIFDGASVDTCTDGRSDGYRWGCTATNFDDKKYGCPCPNADTAI---GNSQDDPC 346
 QY 132 HPFLYNNHNYTDTCTSEGRDNMKKCGTTONTYADOKFGFCP-----MAHEICTT 183
 Db 347 VFPEFTLGSYSRISYQGRDGLWCATTSNYDTDKKWCPCPRGYSIFLVAHE----- 401
 QY 184 NEGMYRIGDQMDKQDMGMKRCCTCVGNGRGEMTCTIAVSQLRDQCIIVDTITVNVDTFH 243
 Db 402 -----FHSILG-----LDHSSVREALMYRYS-VQD--F 428
 QY 244 KRHEEGHMLNCTCGGGRGRWKCPVDOCDSGTGTFYQIGDSWEKRYHGVRYQCYGR 303
 Db 429 QLHEDD-----VGGIQ---YLYGR 444

QY 304 GIGEMHCOPL-----QTPSSSG---PVEVFTITPSPNSHP 338
 Db 445 GSGEPTPPAPLPTEPQSIPTKASASTEEBEETP-EPTAPB 488

RESULT 15

095J04 PRELIMINARY; PRT; 661 AA.
 AC 095J04;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Gelatinase A.
 GN MMP-2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Enamel organ;
 RA Caron C., Xue J., Bartlett J.D.;
 RT "Localization of Gelatinase A (MMP-2) in developing tooth tissues and
 in vitro amelogelatin hydrolysis".
 RU Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF295805; AAK97133.1; -
 DR HSSP; P39900; 1U1Z.
 DR MEROPS; M10.003; -
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrxin.
 DR InterPro; IPR006026; Nzh_MTpeptidase.
 DR InterPro; IPR006025; Zn_MTpeptidase.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; peptidase_M10; 1.
 DR Pfam; PF03933; peptidase_M10_N; 1.
 DR PRINTS; PRO00138; FNTYPEII.
 DR PRINTS; PRO0013; MATRXIN.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00130; HX; 4.
 DR SMART; SM00235; ZNMG; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KM Hydrolyase; Metal-binding; Metalloprotease; Protease; Zinc.
 SQ SEQUENCE 661 AA; 73669 MW; 41CD448BD72DC2 CRC64;

Query Match 18.9%; Score 378.5; DB 6; Length 661;
 Best Local Similarity 37.9%; Pred. No. 3, 1e-27;
 Matches 78; Conservative 30; Mismatches 77; Indels 21; Gaps 6;

QY 55 ETAVTQYGGNSNGEPCVLPPTVNGRTFYCTTBGRDGLHWCSTTSNYEDQKSFCTD 114
 Db 218 EGQVRYVYGYGNADGEYCKFPSPFNGKEXYNSCTDGRSDGFLWCSTYVFDKGYGFC-P 276
 QY 115 HTVAVQIRGNSNGALCHPEFLYNNHNTDCTSGRPRDMMKCGTQNYADQKFGPCPM 174
 Db 277 HEALP-TWGGNADQPCPKFPFQGTSYNSCTTBGRDGYRWCCTEDYDRDKYGFCE 335
 QY 175 AAHEEICTTNEG------MYRIGDQMDKQDMGMHMRCTCVGNRGEWTCIA--YSOLR 226
 Db 336 TAMSTVGNSRGCACVFPFTFLGNKHS-----CTSAGRSDGKLMCAITANYDDDR 386
 QY 227 DQCLVDITVAVNDTFKRRHEGHML 252
 Db 387 KMGFCPDQGYSL--FLVAHHEFGHAM 410

Search completed: November 28, 2003, 15:01:35
 Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:11 ; Search time 21 Seconds

(Without alignments)
1570.755 Million cell updates/sec

Title: US-09-934-706-1

Perfect score: 2002

Sequence: 1 MAAVYQPPHPQPPFYGHCV.....EVFTETPPQPNHPHQLWE 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1979	98.9	2386	1 FNMU	fibronectin precu
2	1927	96.3	2265	1 FNBO	fibronectin - bovi
3	1877	93.8	2477	2 S14428	fibronectin precu
4	1601	80.0	2481	2 A43908	fibronectin - Afri
5	961	48.0	190	2 I51279	fibronectin - east
6	396.5	19.8	707	1 A53796	gelatinase B (EC 3
7	393	19.6	708	2 UC4364	gelatinase B (EC 3
8	386.5	19.3	662	2 S70365	gelatinase A (EC 3
9	385.5	19.3	662	2 A42496	gelatinase A (EC 3
10	385.5	19.3	662	2 S34780	gelatinase A (EC 3
11	382.5	19.1	660	1 A28153	gelatinase A (EC 3
12	382.5	19.1	663	1 S46492	gelatinase A (EC 3
13	382	19.1	708	2 S62907	gelatinase B (EC 3
14	382	19.1	730	1 I52580	gelatinase B (EC 3
15	382	19.1	730	1 UC1456	gelatinase B (EC 3
16	381	19.0	712	1 A46031	gelatinase B (EC 3
17	374	18.7	707	1 A34458	gelatinase B (EC 3
18	203	10.1	1326	2 B56385	secretory phosphol
19	203	10.1	1465	2 A56385	secretory phosphol
20	202	10.1	1455	2 A48925	mannose receptor p
21	195.5	9.8	1463	2 A53210	phospholipase A2 r
22	193	9.6	1456	2 A36563	mannose receptor p
23	189.5	9.5	1458	2 A49707	phospholipase A2 r
24	187	9.3	1479	2 T42710	mannose receptor,
25	181	9.0	121	2 S58424	seminal plasma pro
26	180.5	9.0	1487	2 S48719	phospholipase-A(2)
27	175.5	8.8	105	2 A58837	DH sperm surface
28	170	8.5	655	1 A46688	hepatocyte growth
29	166.5	8.3	115	2 A29156	seminal fluid prot

30	165	8.2	615	1 KFHU12	coagulation factor
31	164.5	8.2	134	1 WTBO	seminal fluid prot
32	159	7.9	2482	2 I48922	cation-independent
33	159	7.9	2483	1 A49617	insulin-like growth
34	156.5	7.8	2491	1 A28372	insulin-like growth
35	156.5	7.8	2499	1 A30788	mannose 6-phosphat
36	154	7.7	593	2 S45281	coagulation factor
37	151.5	7.6	2470	2 I50726	cation-independent
38	148.5	7.4	1020	2 A29355	fibronectin - chic
39	144	7.2	603	2 S28841	coagulation factor
40	140.5	7.0	1723	2 S58880	receptor DBC-205 -
41	134.5	6.7	719	2 T00266	hypotheical prote
42	125	6.2	922	2 T23573	hypotheical prote
43	125	6.2	3712	2 I18253	laminin alpha-1 ch
44	122	6.1	551	2 I46709	endothelial leukoc
45	120	6.0	23	2 B43836	fibronectin - rabb

ALIGNMENTS

RESULT 1

FNMU
fibronectin precursor [validated] - human
N;Alternate names: fibronectin splice form ED-A
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 08-Dec-2000
C;Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22;
R;Dean, D.C.; Bowlin, C.L.; Bourgeois, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
A;Title: Cloning and analysis of the promoter region of the human fibronectin gene.
A;Reference number: A26460; PMID:8715578; PMID:3031656
A;Accession: A26460
A;Molecule type: DNA
A;Residues: 1-49 <DEA>
A;Cross-references: GB:M15801; NID:G182686; PIDN:AA53376.1; PID:G553293
R;Paolillo, G.; Hendchiff, C.; Sebastio, G.; Baralle, F.E.
J. Biol. Chem. 261, 2113-2116, 1986
A;Title: Evolution of the fibronectin gene.
A;Reference number: A26284; PMID:8611901; PMID:3003095
A;Accession: A26284
A;Molecule type: DNA
A;Residues: 1447-1540 <OLD>
A;Cross-references: GB:M12549; NID:G182688
A;Note: the authors translated the codon TTC for residue 1494 as Glu
R;Paolillo, G.; Hendchiff, C.; Sebastio, G.; Baralle, F.E.
Nucleic Acids Res. 16, 3545-3557, 1988
A;Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B
A;Reference number: S00848; PMID:88233940; PMID:3375063
A;Accession: S03917
A;Molecule type: DNA
A;Residues: 1594-1767, 'V', 1769-1783 <PAO>
A;Cross-references: EMBL:X07718; NID:G31402
A;Note: the authors translated the codon AAC for residue 1631 as Asp
R;Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
FEBS Lett. 207, 287-291, 1986
A;Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:
A;Reference number: A24854; PMID:87030929; PMID:3770201
A;Accession: A24854
A;Molecule type: DNA
A;Residues: 1992-2147 <VTB>
A;Cross-references: GB:X04530; NID:G31436
R;Gutman, A.; Yamada, K.M.; Kornblith, A.
FEBS Lett. 207, 145-148, 1986
A;Title: Human fibronectin is synthesized as a pre-propolypeptide.
A;Reference number: A24476; PMID:87030890; PMID:3770189
A;Accession: A24476
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-14, 'Q', 16-38 <GUT>
R;Kornblith, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
EMBO J. 4, 1755-1759, 1985
A;Title: Primary structure of human fibronectin: differential splicing may generate at le

A;Reference number: A91008; MUID:85284965; PMID:2992939
A;Accession: A91008
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 32-1344, 1346-2080, 2112-2386 <KOR>
R;Cross-references: GB:X02761
R;Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5866, 1984
A;Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A;Reference number: A93529; MUID:84272258; PMID:6462919
A;Accession: A93529
A;Molecule type: mRNA
A;Residues: 973-2080, 2112-2386 <KO2>
A;Cross-references: GB:X00739
R;Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A;Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a
A;Reference number: A21011; MUID:83290929; PMID:6688418
A;Accession: A21011
A;Molecule type: mRNA
A;Residues: 1434-1537 <OL2>
A;Cross-references: GB:K00055; NID:G182680; PIDN:AAA52459.1; PID:G182683
R;Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A;Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra
A;Reference number: A90495; MUID:85280409; PMID:2992573
A;Accession: A90495
A;Molecule type: mRNA
A;Residues: 1594-2386 <BRR>
A;Cross-references: GB:M10905; NID:G182696; PIDN:AAA52462.1; PID:G182697
R;Umezawa, K.; Kornblith, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A;Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A;Reference number: A22245; MUID:85231203; PMID:2989004
A;Accession: A22245
A;Molecule type: mRNA
A;Residues: 1948-2067 <UME>
A;Cross-references: GB:M27589; NID:G182705; PIDN:AAA52465.1; PID:G182706
A;Accession: B22245
A;Molecule type: mRNA
A;Residues: 1975-1991, 2017-2039 <UM2>
A;Cross-references: GB:M27590
R;Sekiguchi, K.; Kios, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A;Title: Human liver fibronectin complementary DNAs: identification of two different mes
A;Reference number: I52394; MUID:87026578; PMID:3021206
A;Accession: I52394
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: mRNA
A;Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 <SEK>
A;Cross-references: GB:M14060; NID:G182701; PIDN:AAA52464.1; PID:G182704
R;Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A;Reference number: A21165; MUID:83221567; PMID:6304699
A;Accession: A21165
A;Molecule type: mRNA
A;Residues: 2291-2386 <KO3>
A;Cross-references: GB:K00789; NID:G182681; PIDN:AAA52460.1; PID:G182684
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 258, 12670-12674, 1983
A;Title: Primary structure of human plasma fibronectin.
A;Reference number: A92398; MUID:84032463; PMID:6630202
A;Accession: A92398
A;Molecule type: protein
A;Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>
R;Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A;Title: Further characterization of the binding of fibronectin to gelatin reveals the F
A;Reference number: S34791; MUID:99312001; PMID:8323285
A;Accession: S34791
A;Molecule type: protein
A;Residues: 291-300, 551-560 <GAR2>

R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3552418
A;Accession: A60904
A;Molecule type: protein
A;Residues: 293-301 <GRI>
R;Calaycay, J.; Pande, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A;Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human p
A;Reference number: A23901; MUID:6608277; PMID:3900070
A;Accession: A23901
A;Molecule type: protein
A;Residues: 616-677, 'Q', 679-703, 'PR' <CAL>
R;Piereschbacher, M.D.; Ruoslahti, E.; Sundell, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A;Title: The cell attachment domain of fibronectin. Determination of the primary structu
A;Reference number: A92386; MUID:82265604; PMID:7050098
A;Accession: A92386
A;Molecule type: protein
A;Residues: 1441-1548 <PIE>
A;Note: residues 1524-1527 are responsible for the cell-binding activity
R;Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A;Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dome
A;Reference number: A32517; MUID:87241275; PMID:3593220
A;Accession: A32517
A;Molecule type: protein
A;Residues: 1589-1630, 'T', 1722-2058 <GAR3>
R;Trittschel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pande
Biochem. J. 274, 731-738, 1991
A;Title: Human plasma fibronectin. Demonstration of structural differences between the A-
A;Reference number: S14357; MUID:91190085; PMID:2012601
A;Accession: S14357
A;Molecule type: protein
A;Residues: 1614-1630, 'T', 1722-2081, 2113-2244 <TRB>
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A;Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dalt
A;Reference number: A23891; MUID:85261459; PMID:4019516
A;Accession: A23891
A;Molecule type: protein
A;Residues: 2071-2080, 2112-2356 <GAR4>
C;Comment: The extra domain and connecting strand 3 are subject to developmental and tise
C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
action, and transformation.
C;Genetics:
A;Gene: GDB:FNI
A;Cross-references: GDB:119135; OMIM:135600
A;Map position: 2q34-2q34
A;Intons: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat
C;Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicati
F;1-6/Domain: signal sequence #status predicted <SIG>
F;27-31/Domain: propeptide #status predicted <PRO>
F;32-2386/Product: fibronectin #status experimental <AMT>
F;52-87/Domain: fibrin and heparin binding <FBH>
F;52-272/Domain: fibrin and heparin binding <FBH>
F;97-135/Domain: fibronectin type I repeat homology <1F1>
F;141-179/Domain: fibronectin type I repeat homology <1F2>
F;186-225/Domain: fibronectin type I repeat homology <1F3>
F;231-270/Domain: fibronectin type I repeat homology <1F4>
F;308-608/Domain: collagen binding <CBR>
F;308-342/Domain: fibronectin type I repeat homology <1F5>
F;360-401/Domain: fibronectin type II repeat homology <2F1>
F;420-461/Domain: fibronectin type II repeat homology <2F2>
F;470-508/Domain: fibronectin type I repeat homology <1F7>
F;518-555/Domain: fibronectin type I repeat homology <1F8>
F;561-599/Domain: fibronectin type I repeat homology <1F9>
F;609-692/Domain: fibronectin type III repeat homology <3FA>
F;616-706/Domain: heparin binding <HRB>
F;719-801/Domain: fibronectin type III repeat homology <3FB>
F;810-891/Domain: fibronectin type III repeat homology <3FC>

F;66-104/Domain: fibronectin type I repeat homology <1F2>

303 RGIGEMHCQPLQTYPPSSGPVEVFITETPSQPNSHPIQW 341

561 RGIGEWACQPLQTPDTSQPVQVITETPSQPNSHPIQW 599

A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-2481 <DES>

A:Cross-references: GB:M77820

A:Note: sequence extracted from NCBI backbone (NCBI:P.77473)

C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat

C:Keywords: duplication; extracellular matrix; glycoprotein; heterodimer

F:55-90/Domain: fibronectin type I repeat homology <1F>

F:100-138/Domain: fibronectin type I repeat homology <1F>

F:144-182/Domain: fibronectin type I repeat homology <1F>

F:189-228/Domain: fibronectin type I repeat homology <1F>

F:234-273/Domain: fibronectin type I repeat homology <1F>

F:309-343/Domain: fibronectin type I repeat homology <1F>

F:361-402/Domain: fibronectin type II repeat homology <2F>

F:471-509/Domain: fibronectin type I repeat homology <1F>

F:519-556/Domain: fibronectin type I repeat homology <1F>

F:562-600/Domain: fibronectin type I repeat homology <1F>

F:610-693/Domain: fibronectin type III repeat homology <FN3A>

F:719-801/Domain: fibronectin type III repeat homology <FN3A>

F:810-891/Domain: fibronectin type III repeat homology <FN3C>

F:906-988/Domain: fibronectin type III repeat homology <FN3D>

F:996-1077/Domain: fibronectin type III repeat homology <FN3E>

F:1086-1165/Domain: fibronectin type III repeat homology <FN3F>

F:1173-1258/Domain: fibronectin type III repeat homology <FN3G>

F:1266-1349/Domain: fibronectin type III repeat homology <FN3H>

F:1357-1440/Domain: fibronectin type III repeat homology <FN3I>

F:1448-1530/Domain: fibronectin type III repeat homology <FN3J>

F:1538-1620/Domain: fibronectin type III repeat homology <FN3U>

F:1615-1617/Region: cell attachment (R-G-D) motif

F:1632-1714/Domain: fibronectin type III repeat homology <FN3L>

F:1722-1804/Domain: fibronectin type III repeat homology <FN3M>

F:1812-1894/Domain: fibronectin type III repeat homology <FN3N>

F:1904-1985/Domain: fibronectin type III repeat homology <FN3O>

F:1993-2075/Domain: fibronectin type III repeat homology <FN3P>

F:2197-2277/Domain: fibronectin type III repeat homology <FN3Q>

F:2301-2340/Domain: fibronectin type I repeat homology <1F10>

F:2346-2383/Domain: fibronectin type I repeat homology <1F11>

F:2390-2425/Domain: fibronectin type I repeat homology <1F12>

F:25-81, 79-90, 100-128, 126-138, 144-171, 170-182, 189-218, 216-228, 234-263, 261-273, 309-336, 33

F:2373, 2371-2383, 2390-2416, 2414-2425/Disulfide bonds: #status predicted

F:2459/Disulfide bonds: interchain (to 2463) #status predicted

F:2463/Disulfide bonds: interchain (to 2459) #status predicted

Query Match 80.0%; Score 1601; DB 2; Length 2481;

Best Local Similarity 77.9%; Pred. No. 4.7e-112;

Matches 264; Conservative 41; Mismatches 32; Indels 2; Gaps 1;

3 AAYQOPHPRRPYGHCVTDSGVVYSGMOMLTKQGNKQMLCTCLGNGVSCOEPAVLYQY 62

295 ALQRPD--SOLBPGHCVTDNGVYSLGKMWLTKQSKQMLCTCLGNGVSCOEPAVLYQY 352

63 GGNNGEPVLPFTYNGRTFSCCTEGRODGHLMCSFTTSNYEDOKYSFCTDHTVLYQY 122

353 GGNANBPALPFTTHGKTYSCSTSEBRODQKLMCATTSNYDSDKKYSFCTEDALVLYQY 412

123 GGNNGALCHPPLVNNHNTDCTSEGRDNMKCGTTONYADQKFGCPMAAHEICT 182

413 GGNNGALCHPPLVNNHNTDCTSEGRDNMKCGTTONYADQKFGCPMAAHEICT 472

183 TNGVWYRGSDQDKDQKDHMMKCTGVNGRGEMWTGIAVSOARDCTVNDIYVNDTF 242

473 TNGVWYRGSDQDKDQKDHMMKCTGVNGRGEMWTGIAVSOARDCTVNDIYVNDTF 532

243 HKHEBHGMLNCTCFGGGRGKCDPVDCODSETGTFTYIGDSWEKYVGVYQCYG 302

533 TKLHEBHGMLNCTCFGGGRGKCDPVDCODSETGTFTYIGDSWEKYVGVYQCYG 592

303 KGIQEWHCOPLOTYPSSGVEVFTTTPSQPNHPOM 341

593 KGIQEWHCOPLOTYPSSGVEVFTTTPSQPNHPOM 631

RESULT 5

151279

fibronectin - eastern newt (fragment)

C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999

C:Accession: 151279

R:Nace, J.D.; Tassava, R.A.

Dev. Dyn. 202; 153-164, 1995

A:Title: Examination of fibronectin distribution and its sources in the regenerating newt

A:Reference number: 151279; PMID:95252528; PMID:7734733

A:Accession: 151279

A:Molecule type: translated from GB/EMBL/DBJ

A:Residues: 1-190 <NAC>

A:Cross-references: GB:S76886; NID:914305; PIDN:AA34250.1; PID:914306

C:Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat

F:7-48/Domain: fibronectin type I repeat homology <2F2>

F:57-95/Domain: fibronectin type I repeat homology <1F7>

F:105-142/Domain: fibronectin type I repeat homology <1F8>

F:148-186/Domain: fibronectin type I repeat homology <1F9>

Query Match 48.0%; Score 961; DB 2; Length 190;

Best Local Similarity 85.8%; Pred. No. 3.4e-65;

Matches 163; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

125 NSNGALCHPPLVNNHNTDCTSEGRDNMKCGTTONYADQKFGCPMAAHEICTTN 184

1 NSNGALCHPPLVNNHNTDCTSEGRDNMKCGTTONYADQKFGCPMAAHEICTTN 60

185 EGVYRIGDQWQKDHMMKCTGVNGRGEMWTGIAVSOARDCTVNDIYVNDTFHK 244

61 EGVYRIGDQWQKDHMMKCTGVNGRGEMWTGIAVSOARDCTVNDIYVNDTFHK 120

245 RHEBHGMLNCTCFGGGRGKCDPVDCODSETGTFTYIGDSWEKYVGVYQCYG 304

121 RHEBHGMLNCTCFGGGRGKCDPVDCODSETGTFTYIGDSWEKYVGVYQCYG 180

305 IGEWHCOPLO 314

181 IGEWHCOPLO 190

RESULT 6

A53796

gelatinase B (EC 3.4.24.35), precursor - rabbit

N:Alternate names: 92K matrix metalloproteinase; 92K type IV collagenase; matrix metallo

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A53796; A55398

R:Tezuka, K.; Nemoto, K.; Tezuka, Y.; Sato, T.; Ikeda, Y.; Kobori, M.; Kawashima, H.; Egi

J. Biol. Chem. 269, 15006-15009, 1994

A:Title: Identification of matrix metalloproteinase 9 in rabbit osteoclasts.

A:Reference number: A53796; PMID:94253056; PMID:8195136

A:Accession: A53796

A:Molecule type: mRNA

A:Residues: 1707 <TEZ>

A:Cross-references: GB:D26514; NID:9499372; PIDN:BA05520.1; PID:9499373

A:Experimental source: osteoclasts

R:Finl, M.E.; Bartlett, J.D.; Matsubara, M.; Rinehart, W.B.; Moody, M.K.; Girard, M.T.; R

J. Biol. Chem. 269, 28620-28628, 1994

A:Title: The rabbit gene for 92-kDa matrix metalloproteinase. Role of AP1 and AP2 in cel

A:Reference number: A55398; PMID:95050662; PMID:7961810

A:Accession: A55398

A:Molecule type: translation not shown

A:Status: translation not shown

A:Residues: 1-75, 'P', '77-99', 'ASR', '103-171 <FIN>

A:Cross-references: GB:L36050; NID:9535714; PIDN:AAA64350.1; PID:9535715

C:Genetics: 46/3; 124/2

A:Initiators: 46/3; 124/2

C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C:Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-106/Domain: activation peptide #status predicted <PRO>

F:107-707/Product: 91K neutrophil gelatinase B #status predicted <MAT>
F:230-271/Domains: fibronectin type II repeat homology <2F9>
F:288-329/Domains: fibronectin type II repeat homology <2F8>
F:347-388/Domains: fibronectin type II repeat homology <2F1>
F:510-704/Domains: hemopexin repeat homology <PXX>
F:188,120,127/Binding site: carbohydrate (asn) (covalent) #status predicted
F:99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:402/Active site: Glu #status predicted

Query Match 19.8%; Score 396.5; DB 1; Length 707;
Best Local Similarity 45.4%; Pred. No. 3.1e-22;
Matches 79; Conservative 23; Mismatches 49; Indels 23; Gaps 6;

QY 16 YGHCVTDSGVVSYGVGMWLTQGNKMLCTGICGNGVSCQETAVIQTGYGNGEPCVLPF 75
Db 241 YTACTTGG--RSDGMAMCSTTADYD---TDRRFGFCSESLYIQ--DGNMDGRPCPEPF 292
QY 76 TYNGRTYSCCTTEGRDGHLMCSTTSNVEQDKYSFC--TDHYVLVOTRGNSNGALCH 132
Db 293 IFQGRYTSACTTDRSDGRHRCATTAASYDKLXGFCPTRADSTVY---GNSAGELCV 348
QY 133 FPFLLNNHNYTDCSEGRDMKMGCTTQNYADAKRECFE-----MAHE 178
Db 349 PPFVFLGKYSCTSEGRDRMLWCATTSNPDSDKMGCFCDKGYSLFLVAHE 402

RESULT 7

JC4364
gelatinase B (EC 3.4.24.35) precursor - rat
N:Alternate names: 92-kDa type IV collagenase; matrix metalloproteinase 9 (MMP9)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999
C/Accession: J04364
R:Okada, A.; Santavirta, M.; Baeset, P.
Gene 164, 317-321, 1995.
A:Title: The cDNA cloning and expression of the gene encoding rat gelatinase B.
A:Reference number: J04364; MUID:9609602; PMID:7590350
A/Accession: J04364
A:Molecule type: mRNA
A:Residues: 1-708 <OKA>
A:Cross-references: CB:U24441; NID:g1173505; PIDN:AAA9911.1; PID:g1173506
A:Experimental source: Skin wounds
C:Comment: This enzyme belongs to the matrix metalloproteinase family, proteolytic enzyme
C/Genetics:
A:Gene: gelB
C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C/Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:1-24/Domains: signal sequence #status predicted <SIG>
F:25-708/Product: progelatinase B #status predicted <PRO>
F:25-107/Domains: activation peptide #status predicted <ACT>
F:108-708/Product: gelatinase B #status predicted <MAT>
F:214-389/Region: collagen binding #status predicted
F:231-271/Domains: fibronectin type II repeat homology <2F1>
F:289-310/Domains: fibronectin type II repeat homology <2F2>
F:348-389/Domains: fibronectin type II repeat homology <2F3>
F:514-707/Domains: hemopexin repeat homology <PXX>
F:139,121/Binding site: carbohydrate (asn) (covalent) #status predicted
F:100,402,406,412/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted
F:403/Active site: Glu #status predicted
F:519-707/Disulfide bonds: #status predicted

Query Match 19.6%; Score 393; DB 2; Length 708;
Best Local Similarity 31.8%; Pred. No. 5.7e-22;
Matches 98; Conservative 35; Mismatches 107; Indels 68; Gaps 12;

QY 47 LGNGVSCQETAVIQTGYGNGEPCVLPFTYNGRTYSCCTTEGRDGHLMCSTTSNVEOD 106
Db 213 LGKG-----AVPTTFGNANGACHPFTFGESYSLCTDGRNDGKPMCGTTADYDT 266
QY 107 QKYSFCTDHTVLVOTRGNSNGALCHPFLYNNHNYTDCSEGRDMKMGCTTQNYADAD 166

Db 267 RKYGFPCSEN--LYTEHGNDGKRCVPPFIFBGHSYACTTKGRSDGRCATTANPDOD 324
QY 167 OKFGFCMAAHEELCTTNE--GVM-----YIIGDQWDQOHMGHMRCTCGNGR--GEWT 218
Db 325 KLYGFCPTRADVTVTGNNSGEMCVPPFVLGKYS-----CTGEGSDRLW 373
QY 219 CIAYSQD---RDQCIVDITVYVNDTFPKRHEEGHMLNCTCFQGRGRMKCDPVQOCDS 275
Db 374 CATTSNFDADKKMGFCPDQGYSL--FLVAHEFGHALG-----LDHSSVP 416
QY 276 ET-----GTRYQIGDSMEKTVHGRYQCYCGRGIGMHCOPLOTYSSGSPVEVFTTET 330
Db 417 EALMYPMYHHEDSPLHEDDIKGIQ---HDYGRG-----SKDPPRPATTA 460
QY 331 PSONSHP 338
Db 461 EPQTPAP 468

RESULT 8

S70365
gelatinase A (EC 3.4.24.24) precursor - rabbit
N:Alternate names: matrix metalloproteinase-2; type IV collagenase
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C/Accession: S70365
R:Matsuno, S.; Katoh, M.; Watanabe, T.; Masuno, Y.
Biochim. Biophys. Acta 1307, 137-139, 1996
A:Title: Molecular cloning of rabbit matrix metalloproteinase-2 and its broad expression
A:Reference number: S70365; MUID:96283805; PMID:8679695
A/Accession: S70365
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-662 <MAT>
A:Cross-references: EMBL:D63579; NID:g944816; PIDN:BA09796.1; PID:g944817
C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:233-274/Domains: fibronectin type II repeat homology <2F1>
F:291-332/Domains: fibronectin type II repeat homology <2F2>
F:349-390/Domains: fibronectin type II repeat homology <2F3>
F:465-662/Domains: hemopexin repeat homology <PXX>
F:102,403,407,413/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
F:404/Active site: Glu #status predicted

Query Match 19.3%; Score 386.5; DB 2; Length 662;
Best Local Similarity 38.8%; Pred. No. 1.6e-21;
Matches 80; Conservative 29; Mismatches 76; Indels 21; Gaps 6;

QY 55 ETAVTQTYGNSNGEPCVLPFTYNGRTYSCCTTEGRDGHLMCSTTSNVEODKYSFCTD 114
Db 217 EGVVRRKYKGNADQEKFPFLNPKGKYTCTDGRSDGLMCTTTFEKDGKGYGC-P 275
QY 115 HTVLVOTRGNSNGALCHPFLYNNHNYTDCSEGRDMKMGCTTQNYADAKFGFGCPM 174
Db 276 HEALF-TMGGNADQPKFPFRFGTSYSTTEGRDGYRWCCTEDYDRDKKYGCPCE 334
QY 175 AAHEICTTNEG-----MTRIGDQMKQDMGMHMRCTGVNGRGWTCLA---YGQLR 226
Db 335 TMSSTIGNSEGAPCVPPFTFLGKYES-----CTAGSRDGRMKCATSTNYDDDR 385
QY 227 DQCIVDITVYVNDTFPKRHEEGHML 252
Db 386 KWGFCPDQGYSL--FLVAHEFGHAM 409

RESULT 9

A42496
gelatinase A (EC 3.4.24.24) precursor - mouse
N:Alternate names: collagenase type IV, 72K
C:Species: Mus musculus (house mouse)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999

C/Accession: A42496
 R.Reponen, P.; Sahlgren, C.; Huhtala, P.; Hurskainen, T.; Thesleff, I.; Trygsvaen, K.
 J. Biol. Chem. 267, 7856-7862, 1992
 A/Title: Molecular cloning of murine 72-kDa type IV collagenase and its expression during
 A/Reference number: A42496, MUID:92218452, PMID:1373140
 A/Accession: A42496
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-662 <REP>
 A/Cross-references: GB:M84324, NID:9198465, PIDN:AAA9338.1, PID:9198466
 A/Note: sequence extracted from NCBI backbone (NCBI:96943, NCBI:96945)
 C/Suprafamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
 C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F/233-274/Domain: fibronectin type II repeat homology <2P1>
 F/291-332/Domain: fibronectin type II repeat homology <2P2>
 F/349-390/Domain: fibronectin type II repeat homology <2P3>
 F/465-662/Domain: hemopexin repeat homology <P2N>
 F/102,403,407,413/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F/404/Active site: Glu #status predicted

Query Match 19.3%, Score 385.5, DB 2, Length 662,
 Best Local Similarity 38.8%, Pred. No. 1.9e-21;
 Matches 80; Conservative 28; Mismatches 77; Indels 21; Gaps 6;

QY 55 ETAVTQTVGNSNGEPCVLPFTYNGRTFYSCTEGRQDHLWCSSTSYEODOKYSPFCD 114
 DB 21 EQQVAVKYGNDGECYCKPFLFNGREYSSCTDGRSDGFLWCSSTYNEKOKYGF-C-P 275
 QY 115 HTVLVOTRGNSNGALCHPFLYNNHNYDCTSEGRDMMKMGCTTONTADQKFGFCPM 174
 DB 276 HNALF-TWGNMADGQCKPFRFGTSYNSCTTEGTDGYRNGCTTEDYDRDKYGFCE 334
 QY 175 AAHEBICITTEGV---MYRIGDQDKQDHGMHMRCTCVNGSGEWTGIA---YSQIR 226
 DB 335 TMSVTVGNSGEGAPCVFPFTFLGNKYES-----CTSAGRNDGKWCATTNYDDDR 385
 QY 227 DQCIYDDITVYNNDFHKKHEBGMHL 252
 DB 386 KMGFCPDGYSL-FLVAABFGHAM 409

RESULT 10
 S34780
 gelatinase A (EC 3.4.24.24) precursor - rat
 N/Alternate names: collagenase type IV
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 22-Jun-1999
 C/Accession: S34780, S32525
 R.Lovett, D.H.
 submitted to the EMBL Data Library, June 1993
 A/Reference number: S34780
 A/Accession: S34780
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-662 <LOV>
 A/Cross-references: EMBL:X71466, NID:9311750, PIDN:CAA5083.1, PID:9854415
 R/Marti, H.P.; McNeill, L.; Davies, M.; Martin, J.; Lovett, D.H.
 Biochem. J. 291, 441-446, 1993
 A/Title: Homology cloning of rat 72 kDa type IV collagenase: cytokine and second-messen
 A/Reference number: S32525, MUID:93249363, PMID:7916617
 A/Accession: S32525
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 'R', 27-662 <MAR>
 A/Cross-references: EMBL:X71466
 C/Suprafamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
 C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F/233-274/Domain: fibronectin type II repeat homology <2P1>
 F/291-332/Domain: fibronectin type II repeat homology <2P2>
 F/349-390/Domain: fibronectin type II repeat homology <2P3>
 F/465-662/Domain: hemopexin repeat homology <P2N>
 F/102,403,407,413/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F/403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
 F/404/Active site: Glu #status predicted

Query Match 19.3%, Score 385.5, DB 2, Length 662,
 Best Local Similarity 38.8%, Pred. No. 1.9e-21;
 Matches 80; Conservative 28; Mismatches 77; Indels 21; Gaps 6;

QY 55 ETAVTQTVGNSNGEPCVLPFTYNGRTFYSCTEGRQDHLWCSSTSYEODOKYSPFCD 114
 DB 21 EQQVAVKYGNDGECYCKPFLFNGREYSSCTDGRSDGFLWCSSTYNEKOKYGF-C-P 275
 QY 115 HTVLVOTRGNSNGALCHPFLYNNHNYDCTSEGRDMMKMGCTTONTADQKFGFCPM 174
 DB 276 HNALF-TWGNMADGQCKPFRFGTSYNSCTTEGTDGYRNGCTTEDYDRDKYGFCE 334
 QY 175 AAHEBICITTEGV---MYRIGDQDKQDHGMHMRCTCVNGSGEWTGIA---YSQIR 226
 DB 335 TMSVTVGNSGEGAPCVFPFTFLGNKYES-----CTSAGRNDGKWCATTNYDDDR 385
 QY 227 DQCIYDDITVYNNDFHKKHEBGMHL 252
 DB 386 KMGFCPDGYSL-FLVAABFGHAM 409

RESULT 11
 A28153
 gelatinase A (EC 3.4.24.24) precursor - human
 N/Alternate names: collagenase type IV, matrix metalloproteinase 2 (MMP2); progelatinase
 C/Species: Homo sapiens (man)
 C/Date: 28-Aug-1989 #sequence_revision 07-Jul-1995 #text_change 18-Jun-1999
 C/Accession: A28153; A34202; A42225; A60187; S13658; S34336; A11480; S4432; A61498; S55
 R/Collier, I.E.; Wilhelm, S.M.; Eissen, A.Z.; Warner, B.L.; Grant, G.A.; Seltzer, J.L.; K
 J. Biol. Chem. 263, 6579-6587, 1988
 A/Title: H-ras oncogene-transformed human bronchial epithelial cells (TBE-1) secrete a si
 A/Reference number: A28153; MUID:88198218; PMID:2834383
 A/Accession: A28153
 A/Molecule type: mRNA
 A/Residues: 30-660 <COL>
 A/Cross-references: GB:J03210, NID:9180670, PIDN:AAA35701.1, PID:9180671
 R/Huhtala, P.; Eddy, R.L.; Fan, Y.S.; Byers, M.G.; Shows, T.B.; Trygsvaen, K.
 Genomics 6, 554-559, 1990
 A/Title: Completion of the primary structure of the human type IV collagenase preprocenzym
 A/Reference number: A34202; MUID:90228972; PMID:2158484
 A/Accession: A34202
 A/Molecule type: DNA
 A/Residues: 1-51 <HU2>
 A/Cross-references: GB:M33789, NID:9180600, PIDN:AAA52027.1; PID:9180601
 R/Huhtala, P.; Chow, L.T.; Trygsvaen, K.
 J. Biol. Chem. 265, 11077-11082, 1990
 A/Title: Structure of the human type IV collagenase gene.
 A/Reference number: A42225; MUID:90293047; PMID:2162831
 A/Accession: A42225
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-51;220-393 <HUB>
 A/Cross-references: GB:M55593; GB:J05471; NID:9180614; PIDN:AAA52028.1; PID:9180616
 A/Note: neither the complete amino acid nor the complete nucleotide sequence is given in
 R/Frisch, S.M.; Reich, R.; Collier, I.E.; Genrich, L.T.; Martin, G.; Goldberg, G.I.
 Oncogene 5, 75-83, 1990
 A/Title: Adenovirus E1A represses protease gene expression and inhibits metastasis of hum
 A/Reference number: A60187; MUID:90206614; PMID:2157183
 A/Accession: A60187
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-58 <PRI>
 R/Okada, Y.; Morimoto, T.; Enghild, J.J.; Suzuki, K.; Yasui, A.; Nakanishi, I.; Salvesen,
 Eur. J. Biochem. 194, 721-730, 1990
 A/Title: Matrix metalloproteinase 2 from human rheumatoid synovial fibroblasts. Purificat
 A/Reference number: S13858; MUID:91099351; PMID:2269296
 A/Accession: S13858
 A/Molecule type: protein
 A/Residues: 30-45;110-124 <OKA>
 R/Crabbe, T.; Ioannou, C.; Docherty, A.J.P.

Eur. J. Biochem. 218, 431-438, 1993
 A;Title: Human procollagenase A can be activated by autolysis at a rate that is concentra
 A;Reference number: S39436; MUID:94094834; PMID:8269931
 A;Accession: S39436
 A;Molecule type: protein
 R;Stetler-Stevenson, W.G.; Krutzsch, H.C.; Wacher, M.P.; Margulies, I.M.K.; Liotta, L.A.
 J. Biol. Chem. 264, 1353-1356, 1989
 A;Title: The activation of human type IV collagenase proenzyme. Sequence identification
 A;Reference number: A31480; MUID:89109136; PMID:2536363
 A;Accession: A31480
 A;Molecule type: protein
 A;Residues: 110-123 <STP>
 R;Crabbe, T.J.; Smith, B.; O'Connell, J.; Docherty, A.
 FEBS Lett. 345, 14-16, 1994
 A;Title: Human procollagenase A can be activated by matrixlysin.
 A;Reference number: S44432; MUID:94252395; PMID:8194591
 A;Accession: S44432
 A;Molecule type: protein
 A;Residues: 110-115 <CRA>
 R;Brown, D.; Chwa, M.; Escobar, M.; Kenney, M.C.
 Exp. Eye Res. 52, 5-16, 1991
 A;Title: Characterization of the major matrix degrading metalloproteinase of human corne
 A;Reference number: A61498; MUID:91330998; PMID:1868885
 A;Accession: A61498
 A;Molecule type: protein
 A;Residues: 'X', '31', 'X', '33-46', 'X', '48-50', 'Q' <BRO>
 A;Experimental source: corneal stroma
 R;Ritch, Y.; Blinner, S.; Nagase, H.
 Biochem. J. 308, 645-651, 1995
 A;Title: Steps involved in activation of the complex of pro-matrix metalloproteinase 2
 A;Reference number: S55327; MUID:95290003; PMID:7772054
 A;Accession: S55327
 A;Molecule type: protein
 A;Residues: 110-114 <ITO>
 C;Genetics:
 A;Gene: GDB:MMP2, CLG4; CLG4A
 A;Cross-references: GDB:120592; OMIM:120360
 A;Map position: 16q13-16q13
 A;Intons: 51/3; 127/2; 178/1; 220/1; 278/1; 336/1; 394/1; 446/1; 491/2; 537/1; 590/2; 6
 C;Function:
 A;Description: proteolytic cleavage of gelatin type I and collagen types IV, V, VII, and
 C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
 C;Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
 F;1-29/Domin: signal sequence #status predicted <SIG>
 F;30-660/Product: procollagenase A #status predicted <PRO>
 F;30-109/Domin: activation peptide #status predicted <ACT>
 F;70-219,394-446/Domin: matrix metalloproteinase homology #status atypical <MMP>
 F;110-660/Product: gelatinase A #status predicted <MAT>
 F;233-390/Region: collagen binding #status predicted
 F;233-374/Domin: fibronectin type II repeat homology <2F1>
 F;291-332/Domin: fibronectin type II repeat homology <2F2>
 F;349-390/Domin: fibronectin type II repeat homology <2F3>
 F;463-660/Domin: hemopexin repeat homology <PXN>
 F;102,403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
 F;403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
 F;404/Active site: Glu #status predicted
 F;469-660/Dissulfide bonds: #status predicted
 F;573,642/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 19.1%; Score 382.5; DB 1; Length 660;
 Best Local Similarity 38.3%; Pred. No. 3.2e-21;
 Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;
 QY 55 ETAVTVYGGNSNPECVLPFTYNGRFFVSTTGRDGHLMWSTTSNYEDOKYSCTD 114
 DB 217 EGVVARKYKYNADSEYCKPFLFNGKYNSTDTGRSGFLMCGSTYVFEKDGKYGFC-P 275
 QY 115 HTVLVQTRGNSNGALCHFPFLYNNHNYTDCSEGRDNMKWCGTTONYDADOKFGFCPM 174
 DB 276 HEALF-TMGNAEBOQPCFPFRFOGTSTSDCTTGRDGYKWCCTTEDYDOKKYGFCPE 334
 QY 175 AAHEICTTNEG-V-----MYRIGDQMDKQHDGMHMRCTGVNGRGEGWTCTIA---YSQLR 226

Db 335 TAMSTVGNSEGAPCVFPFFFLNKKYSES-----CTSAGRSDDGKMCATTANYDDDR 385
 QY 227 DQCIVDITVYNDTFPKHREEGHML 252
 Db 386 KWGFCPDQGYSL--FLVAHAEFGHAM 409
 RESULT 12
 S46492
 gelatinase A (EC 3.4.24.24) precursor - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: S46492
 R;Almes, R.T.; French, D.L.; Quigley, J.P.
 Biochem. J. 300, 729-736, 1994
 A;Title: Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from chicken embryo f
 A;Reference number: S46492; MUID:94280397; PMID:8010954
 A;Accession: S46492
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-663 <AIM>
 A;Cross-references: EMBL:U07775; NID:G504475; PID:AA19596.1; PID:G504476
 A;Note: in the authors' translation 205-Asp is shown after residue 201 and, consequently,
 C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
 C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F;67-216,391-443/Domin: matrix metalloproteinase homology #status atypical <MMP>
 F;230-271/Domin: fibronectin type II repeat homology <2F1>
 F;230-387/Domin: fibronectin type II repeat homology <2F2>
 F;346-387/Domin: fibronectin type II repeat homology <2F3>
 F;466-663/Domin: hemopexin repeat homology <PXN>
 F;99,400,404,410/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status i
 F;400,404,410/Binding site: zinc, catalytic (His) (active) #status predicted
 F;401/Active site: Glu #status predicted
 Query Match 19.1%; Score 382.5; DB 1; Length 663;
 Best Local Similarity 37.0%; Pred. No. 3.3e-21;
 Matches 77; Conservative 31; Mismatches 75; Indels 25; Gaps 6;
 QY 55 ETAVTVYGGNSNPECVLPFTYNGRFFVSTTGRDGHLMWSTTSNYEDOKYSCTD 114
 DB 214 EGVVARKYKYNADSEYCKPFLFNGKYNSTDTGRSGFLMCGSTYVFEKDGKYGFCPH 273
 QY 115 HTVLVQTRGNSNGALCHFPFLYNNHNYTDCSEGRDNMKWCGTTONYDADOKFGFCPM 174
 DB 274 ESLE-TMGNGDGOQPCFPFRFOGTSTSDCTTGRDGYKWCCTTEDYDOKKYGFCPE 331
 QY 175 AAHEICTTNEG-V-----MYRIGDQMDKQHDGMHMRCTGVNGRGEGWTCTIA--SQLRDQ- 228
 DB 332 TAMSTVGNSEGAPCVFPFFFLNKKYDS-----CTSAGRNDGLMCASSTSSYDDDR 382
 QY 229 ----CIVDITVYNDTFPKHREEGHML 252
 DB 383 KWGFC--PDQGYSL--FLVAHAEFGHAM 406
 RESULT 13
 S62907
 gelatinase B (EC 3.4.24.35) precursor - rat
 N;Alternate names: collagenase type IV
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 30-Sep-2001
 C;Accession: S62907; S72371
 R;Xia, Y.; Garcia, G.; Chen, S.; Wilson, C.B.; Feng, L.
 FEBS Lett. 382, 285-288, 1996
 A;Title: Cloning of rat 92-kDa type IV collagenase and expression of an active recombinar
 A;Reference number: S62907; MUID:96184505; PMID:8605986
 A;Accession: S62907
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-708 <XIA>
 A;Cross-references: EMBL:U36476
 R;Feng, L.

submitted to the EMBL Data Library, September 1995
A:Reference number: S72371

A:Accession: S72371

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-127, 'S', 129-708 <FEN>

A:Cross-references: EMBL:U6476; NID:g1022783; PIDN:AAB01721.1; PID:g1022784

C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C:Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase

F:1-19/DNA: signal sequence #status predicted <SIG>

F:20-107/DNA: propeptide #status predicted <PRO>

F:58-217.393-445/DNA: activation peptide #status predicted <ACT>

F:108-708/Region: gelatinase A #status predicted <MAT>

F:214-389/Region: collagen binding #status predicted

F:231-272/DNA: fibronectin type II repeat homology <2F1>

F:289-330/DNA: fibronectin type II repeat homology <2F2>

F:348-389/DNA: fibronectin type II repeat homology <2F3>

F:514-707/DNA: hemopexin repeat homology <PXN>

F:100-402.406-412/Binding site: zinc, catalytic (His, His, His, His) (inhibited) #status

F:403/Active site: Glu #status predicted

F:519-707/Disulfide bonds: #status predicted

Query Match 19.1%; Score 382; DB 2; Length 708;
Best Local Similarity 38.1%; Pred. No. 3, 8e-21;
Matches 82; Conservative 25; Mismatches 80; Indels 28; Gaps 7;

47 LGNGVSCQETAVYQYVGNNGEPCVLPFTYNGRTFYSCCTEGRODGLMCSTTSNYEOD 106

213 LGKG-----AVPTVYGNMNGAPCHFPFTEGRSYLCTDGRNDGKPMCGTTADYD 266

107 QKXSFCTDHTVLYVOTRGNGNGALCHFPFLNNHNYDCTSEGRDMMKCGTTQNTAD 166

267 RKYGFCSEN--LYTEGNDGKRCVPLFTEGHSYACCTKGRSDRYCATTAANDOD 324

167 QKGFCEPMABHEICTTNE-GVM-----YRIGDQWDQHMGMRCCTCGNGSGEWTCI 220

325 KAGGFCRTADVVTGNSGEMKVPFVFLGKQY-----TCTSEGRSDRLMCA 375

221 AYSQ-----RDQCIYDITTYNNVDTFHKRHEGHML 252

376 TTSNFADKKWGCPCDQGYSL--FLVAHEFGHML 408

RESULT 14

152580

gelatinase B (EC 3.4.24.35) precursor - mouse

N:Alternate names: collagenase type IV

C:Species: Mus sp. (mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: 152580

R:Grabert, T.; Johnston, J.; Berliner, N.

Blood 82, 3193-3197, 1993

A:Title: Cloning and expression of the cDNA encoding mouse neutrophil gelatinase; demon

A:Reference number: 152580; MUID:9403534; PMID:8219207

A:Accession: 152580

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-730 <RES>

A:Cross-references: GB:S67830; NID:g460863; PIDN:AAB26942.1; PID:g460864

C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C:Keywords: hydrolase; metalloproteinase; zinc; zymogen

F:230-271/DNA: fibronectin type II repeat homology <2F1>

F:288-329/DNA: fibronectin type II repeat homology <2F2>

F:347-388/DNA: fibronectin type II repeat homology <2F3>

F:529-729/DNA: hemopexin repeat homology <PXN>

F:100-401.405-411/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted

F:402/Active site: Glu #status predicted

Query Match 19.1%; Score 382; DB 1; Length 730;

Best Local Similarity 40.1%; Pred. No. 3, 9e-21;

Matches 79; Conservative 26; Mismatches 52; Indels 40; Gaps 8;

16 YGHCTDSDGVVSVGMQMLKT-----QGNKQMLCTGLGNGVSCQETAVYQYVGNNGEPC 70

241 YSACTTDG--RNDGTFWCSCTADYDQGFPCP-----SERLYTE--HNGEGKP 287

71 CVAPFTYNGRTFYSCCTEGRODGLMCSTTSNYEODQKYSFC---IDHTVLYVOTRGNGSN 127

288 CVPFIFTEGRSYACCTKGRSDRYCATTAANDOKLYVFCCTRYADATV-----GQNSA 343

128 GACHPPEFLNNHNYDCTSEGRDMMKCGTTQNTADQKFCPCP-----MAAHE- 178

344 GELCVPPFVFLGKQYSCSTSDGRDRDLMCATTSNEDTDKMGFCPCDQGYSLFLVAHEF 403

179 -----EICTTNEGVMY 189

404 GHALGDHSSVPEALMY 420

RESULT 15

JC1456

gelatinase B (EC 3.4.24.35) precursor - mouse

N:Alternate names: 92K gelatinase; 92K type IV collagenase; matrix metalloproteinase 9

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000

C:Accession: JC1456; S39525; S39526; I48296; S38654

R:Tanaka, H.; Hojo, K.; Yoshida, H.; Yoshida, T.; Sugita, K.

Biochem. Biophys. Res. Commun. 190, 732-740, 1993

A:Title: Molecular cloning and expression of the mouse 105-kDa gelatinase cDNA.

A:Reference number: JC1456; MUID:93176173; PMID:8382489

A:Accession: JC1456

A:Molecule type: mRNA

A:Residues: 1-730 <TRAN>

A:Cross-references: DBJ:D12712; NID:g286079; PIDN:BA02208.1; PID:g286080

R:Maure, S.; Nye, G.; Fiten, P.; van Damme, J.; Opdenacker, G.

Eur. J. Biochem. 218, 129-141, 1993

A:Title: Mouse gelatinase B. cDNA cloning, regulation of expression and glycosylation in

A:Reference number: S39525; MUID:94062823; PMID:8243459

A:Accession: S39525

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-638, 'L', 640-730 <MAS>

A:Cross-references: EMBL:X72794; NID:g433432; PIDN:CAA51314.1; PID:g433433

A:Accession: S39526

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 133-513, 'A', 515-710, 'P', 712-730 <MA2>

A:Cross-references: EMBL:X72795; NID:g433434; PIDN:CAA51315.1; PID:g433435

R:Reponen, P.; Sahlborg, C.; Munaut, C.; Thesleff, I.; Tytgvaason, K.

J. Cell Biol. 124, 1091-1102, 1994

A:Title: High expression of 92-kD type IV collagenase (gelatinase B) in the osteoclast li

A:Reference number: A54476; MUID:94179406; PMID:8132709

A:Accession: I48296

A:Molecule type: mRNA

A:Residues: 1-513, 'A', 515-710, 'P', 712-730 <RES>

A:Cross-references: EMBL:Z27231; NID:g415980; PIDN:CAA81745.1; PID:g415981

C:Gene: CUG4B

A:Intons: 47/3; 124/2; 174/1; 217/1; 275/1; 333/1; 392/1; 444/1; 555/2; 602/1; 652/2; 6

C:Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C:Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase,

F:1-24/DNA: signal sequence #status predicted <SIG>

F:25-730/Product: progelatinase A #status predicted <PRO>

F:108-330/Product: gelatinase A #status predicted <ACT>

F:213-388/Region: collagen binding #status predicted

F:230-271/DNA: fibronectin type II repeat homology <2F1>

F:288-329/DNA: fibronectin type II repeat homology <2F2>

F:347-388/DNA: fibronectin type II repeat homology <2F3>

F:529-729/Region: hemopexin repeat homology <PXN>

F:100-401.405-411/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F:401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted

F:402/Active site: Glu #status predicted

Query Match 19.1%; Score 382; DB 1; Length 730;

Best Local Similarity 40.1%; Pred. No. 3, 9e-21;

F:402/Active site: Glu #status predicted
F:534-729/Disulfide bonds: #status predicted

Query Match 19.1%; Score 382; DB 2; Length 730;
Best Local Similarity 40.1%; Pred. No. 3.9e-21;
Matches 79; Conservative 26; Mismatches 52; Indels 40; Gaps 8;

QY	16	YGHCVTDSGVVSVGMQWLT----	QGNQMQLCTCLGNVSCQETAVTQTYGNSNGEP	70
Db	241	YSACTTDG---RNDGTPWCSTTADYDKDKFGFCP-----	SRLYTE--HGNGEGKP	287
QY	71	CVLPETVNGRTFYSCSTTEGRDGHWCSTSTSNVEDOKYSFC---	TDHTVLVQTRGNSN	127
Db	288	CVPPPIFEGRSYSACTTYGRSDGYRWCATTANYDQDKLYGFCPTFRVDAIV--	GNNSA	343
QY	128	GALCHFPFLYNNHNYTDCTSEGRDNMKMCCTTONYADADOKFGFCP-----	MAAHE-	178
Db	344	GELCVFPFVFLGKQYSSCTSDGRDRLMCATTSNFTDKKMGFCPDQGYSLFLVAHAHF		403
QY	179	-----EICTTNEGVMY	189	
Db	404	GHALGLDHSVPEALMY	420	

Search completed: November 28, 2003, 15:02:08
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:59:11 ; Search time 17 Seconds
(without alignments)

948.833 Million cell updates/sec

Title: US-09-934-706-1

Sequence: 1 MAAVYQPPHPQPPYGHCV.....EVPITETPSPNSHPQWLE 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1984	99.1	2386	1	F1NC_HUMAN
2	1927	96.3	2265	1	F1NC_BOVIN
3	1877	93.8	2477	1	F1NC_RAT
4	1591	79.5	2481	1	F1NC_XENTLA
5	961	48.0	190	1	F1NC_NOVI
6	396.5	19.8	707	1	MM09_RABIT
7	386.5	19.3	662	1	MM02_RABIT
8	385.5	19.3	662	1	MM02_MOUSE
9	385.5	19.3	662	1	MM02_RAT
10	382.5	19.1	660	1	MM02_HUMAN
11	382.5	19.1	663	1	MM02_CHICK
12	382	19.1	708	1	MM09_RAT
13	382	19.1	730	1	MM09_MOUSE
14	381	19.0	712	1	MM09_BOVIN
15	374	18.7	707	1	MM09_HUMAN
16	373	18.6	2477	1	F1NC_MOUSE
17	364.5	18.2	704	1	MM09_CANFA
18	291	14.5	1256	1	F1NC_CHICK
19	210	10.5	1328	1	F1NC_PLEWA
20	200.5	10.0	522	1	F1NC_HORSE
21	196.5	9.8	522	1	F1NC_CANFA
22	195.5	9.8	1463	1	PA2R_BOVIN
23	193	9.7	653	1	GAFA_MOUSE
24	193	9.6	1456	1	MANR_HUMAN
25	190.5	9.5	130	1	SPI_HORSE
26	189.5	9.5	1458	1	PA2R_RABIT
27	178.5	8.9	183	1	SEPA_BOVIN
28	175.5	8.8	130	1	PBI_PIG
29	170	8.5	655	1	HGFA_HUMAN
30	170	8.5	794	1	SEIL_HUMAN
31	165	8.2	615	1	FA12_HUMAN
32	164.5	8.2	134	1	SFP1_BOVIN
33	164.5	8.2	140	1	SFP3_BOVIN

ALIGNMENTS

RESULT 1	ID	F1NC_HUMAN	STANDARD:	PRT: 2386 AA.	
AC	P02751	Q14326: Q9H1B8;			Q92296 mus musculus
DT	21-JUL-1986	(Rel. 01, Created)			O07113 mus musculus
DT	01-NOV-1997	(Rel. 35, Last sequence update)			P11717 homo sapien
DT	15-SEP-2003	(Rel. 42, Last annotation update)			P08169 bos taurus
DE	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).				P98160 bos taurus
GN	FN1 OR FN.				P04962 cavia porce
OS	Homo sapiens (human).				P23730 cavia famli
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				P27113 oryctolagus
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				O00174 drosophila
OX	NCBI_TaxId=9606;				P98164 homo sapien
RN	[1]				P97607 rattus norv
RP	SEQUENCE OF 1-38 FROM N.A.				O88307 m bottlin-
RX	MEDLINE=87030880; PubMed=3770189;				
RA	Gutman A., Yamada K.M., Kornblint A.R.;				
RT	"Human fibronectin is synthesized as a pre-propolypeptide.";				
RL	FEBS Lett. 207:145-148(1986).				
RN	[2]				
RP	SEQUENCE OF 1-49 FROM N.A.				
RX	MEDLINE=87175578; PubMed=3031656;				
RA	Dean D.C., Bowles C.L., Bourgeois S.;				
RT	"Cloning and analysis of the promoter region of the human fibronectin gene.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).				
RN	[3]				
RP	SEQUENCE OF 32-2081 AND 2113-2386 FROM N.A.				
RX	MEDLINE=85284965; PubMed=292939;				
RA	Kornblint A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;				
RT	"Primary structure of human fibronectin: differential splicing may generate at least 10 polypeptides from a single gene.";				
RL	EMBO J. 4:1755-1759(1985).				
RN	[4]				
RP	SEQUENCE OF 973-2081 AND 2113-2386 FROM N.A.				
RX	MEDLINE=84272258; PubMed=6462919;				
RA	Kornblint A.R., Vibe-Pedersen K., Baralle F.E.;				
RT	"Human fibronectin: cell specific alternative mRNA splicing generates polypeptide chains differing in the number of internal repeats.";				
RL	Nucleic Acids Res. 12:5853-5868(1984).				
RN	[5]				
RP	SEQUENCE OF 1594-2386 FROM N.A.				
RX	MEDLINE=85280409; PubMed=2992573;				
RA	Bernard M.P., Kolbe M., Weil D., Chu M.-L.;				
RT	"Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat identifies primary structural domains separated by hypervariable regions.";				
RL	Biochemistry 24:2698-2704(1985).				
RN	[6]				
RP	SEQUENCE OF 32-290.				
RX	MEDLINE=84032463; PubMed=6630202;				
RA	Garcia-Pardo A., Pearlsstein B., Frangione B.;				
RT	"Primary structure of human plasma fibronectin. The 29,000-dalton NH2-terminal domain.";				
RL	J. Biol. Chem. 258:12670-12674(1983).				
RN	[7]				

RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
RX MEDLINE=87080265; PubMed=3024962;
RA Owens R.J., Baralle F.E.;
RT "Mapping the collagen-binding site of human fibronectin by expression
in *Escherichia coli*.";
RL EMBO J. 5:2825-2830(1986).
RN [8]
RP SEQUENCE OF 1441-1548.
RX MEDLINE=82265604; PubMed=7050098;
RA Pletschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;
RT "The cell attachment domain of fibronectin. Determination of the
primary structure.";
RL J. Biol. Chem. 257:9593-9597(1982).
RN [9]
RP SEQUENCE OF 1434-1537 FROM N.A.
RX MEDLINE=83290929; PubMed=6688418;
RA Oldberg A., Linney E., Ruoslahti E.;
RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for
the cell attachment domain in human fibronectin.";
RL J. Biol. Chem. 258:10193-10196(1983).
RN [10]
RP SEQUENCE OF 1448-1540 FROM N.A.
RX MEDLINE=86111901; PubMed=3003095;
RA Oldberg A., Ruoslahti E.;
RT "Evolution of the fibronectin gene. Exon structure of cell attachment
domain.";
RL J. Biol. Chem. 261:2113-2116(1986).
RN [11]
RP SEQUENCE OF 1712-1739 FROM N.A.
RX MEDLINE=87026579; PubMed=3021206;
RA Setiguchi K., Kios A.M., Kizachi K., Yoshitake S., Hakomori S.;
RT "Human liver fibronectin complementary DNAs: identification of two
different messenger RNAs possibly encoding the alpha and beta
subunits of plasma fibronectin.";
RL Biochemistry 25:4936-4941(1986).
RN [12]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Schor S.L., Schor A.M., Seneviratne K., Kay R., Ellis I., Baillie R.,
Clausen J.;
RT "Migration stimulating factor (MSF): a novel transcription variant of
the fibronectin gene.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SUBFATION.
RX MEDLINE=86042625; PubMed=2414772;
RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
RT "Tyrosine sulfation of proteins from the human hepatoma cell line
HepG2.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
RN [14]
RP FBLN1-BINDING SITE.
RX PubMed=1400330;
RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,
Argaves W.S.;
RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding
region of fibronectin.";
RL J. Biol. Chem. 267:20120-20125(1992).
RN [15]
RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
RX MEDLINE=95081153; PubMed=7989369;
RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
RT "Further characterization of the NH2-terminal fibrin-binding site on
fibronectin.";
RL J. Biol. Chem. 269:31938-31945(1994).
RN [16]
RP STRUCTURE BY NMR OF 32-92.
RX MEDLINE=96069779; PubMed=7583666;
RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;
RT "High-resolution structural studies of the factor XIIIa crosslinking
site and the first type I module of fibronectin.";
RL Nat. Struct. Biol. 2:946-950(1995).
RN [17]
RP STRUCTURE BY NMR OF 182-275.

RX MEDLINE=94141923; PubMed=8308892;
RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,
Campbell I.D.;
RT "Solution structure of a pair of fibronectin type I modules with
fibrin binding activity.";
RL J. Mol. Biol. 235:1302-1311(1994).
RN [18]
RP STRUCTURE BY NMR OF 406-464.
RX MEDLINE=98179558; PubMed=9514732;
RA Stich H., Pickford A.R., Potts J.R., Campbell I.D.;
RT "Solution structure of the glycosylated second type 2 module of
fibronectin.";
RL J. Mol. Biol. 276:177-187(1998).
RN [19]
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=9304665; PubMed=1423622;
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;
RT "The three-dimensional structure of the tenth type III module of
fibronectin: an insight into RGD-mediated interactions.";
RL Cell 71:671-678(1992).
RN [20]
RP STRUCTURE BY NMR OF 1447-1540.
RX MEDLINE=92162710; PubMed=1311202;
RA Baron M., Main A.L., Disocoll P.C., Mardon H.J., Boyd J.,
Campbell I.D.;
RT "1H NMR assignment and secondary structure of the cell adhesion type
III module of fibronectin.";
RL Biochemistry 31:2068-2073(1992).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1447-1555.
RX MEDLINE=94166075; PubMed=9120886;
RA Dickinson C.D., Veerapandian B., Dai X.-P., Hamlin R.C., Xiong N.-H.,
Ruoslahti E., Ely K.R.;
RT "Crystal structure of the tenth type III cell adhesion module of
human fibronectin.";
RL J. Mol. Biol. 236:1079-1092(1994).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 1721-1991.
RX MEDLINE=99177162; PubMed=10075919;
RA Sharma A., Askari J.A., Humphries M.J., Jones E.Y., Stuart D.I.;
RT "Crystal structure of a heparin- and integrin-binding segment of human
fibronectin.";
RL EMBO J. 18:1468-1479(1999).
RN [23]
RP FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, ORGANOIZATION, WOUND
HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
variants, connected by 2 disulfide bonds near the carboxyl ends;
to a lesser extent homodimers. Interacts with FBLN1.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
Name=2; IsoId=P02751-1, Sequence=Displayed;
Name=2; Synonyms=MSF-FN70, Migration stimulation factor FN70;
IsoId=P02751-2, Sequence=VSP 003255, VSP 003256, VSP 003257;
CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC -1- PPM: SULFATED.
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC -1- SIMILARITY: Contains 16 fibronectin type III domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

Query Match 99.1%; Score 1984; DB 1; Length 2386;
Best Local Similarity 99.7%; Pred. No. 5,1e-156;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 2 AAVYQPPHPPPPYCHYTDGCVYVSGVMQWMLKTKGNKMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQPPHPPPPYCHYTDGCVYVSGVMQWMLKTKGNKMLCTCLGNGVSCQETAVTQT 350
DB 62 YGNGSGECVLPFTYNGRTFYCTEKGODGLNCKSTSNYQDOKYSCFDHTVLYVT 121
DB 351 YGNGSGECVLPFTYNGRTFYCTEKGODGLNCKSTSNYQDOKYSCFDHTVLYVT 410
QY 122 RGNGSGALCHPFLNNHNYTCTSEGRDNMKCGTQNVADOKPFGCPMAAHEBIC 181
DB 411 QGNGSGALCHPFLNNHNYTCTSEGRDNMKCGTQNVADOKPFGCPMAAHEBIC 470
QY 182 TTNEGVMYRIGDQWDKQHDGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDITVNVDT 241
DB 471 TTNEGVMYRIGDQWDKQHDGMHMRCTCVNGRGEWTCIAYSQLRDQCIYDITVNVDT 530
QY 242 FKRHEEGHMLNCTCGGGRGKCPVQCCDSEGTGTQIGDSWEKTVHGVRQCYCY 301
DB 531 FKRHEEGHMLNCTCGGGRGKCPVQCCDSEGTGTQIGDSWEKTVHGVRQCYCY 590
QY 302 GRGIGEMHCOPLQTPYSSGPVVFITTEPSPNSHPIDW 341
DB 591 GRGIGEMHCOPLQTPYSSGPVVFITTEPSPNSHPIDW 630
```

RESULT 2

FINC BOVIN STANDARD; PRT; 2265 AA.

```
ID F1NC BOVIN STANDARD; PRT; 2265 AA.
AC P07589;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibronectin (FN).
GN FNI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=87054047; PubMed=3780752;
RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin.",
RL Eur. J. Biochem. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=83117805; PubMed=6218503;
RA Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
RA Sahl P., Sottrup-Jensen L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
of internal homology.",
RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
RN [3]
RP SEQUENCE OF 2170-2265 FROM N.A.
RX MEDLINE=83221567; PubMed=6304699;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
fibronectins.",
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OSSONIZATION, WOUND
HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS,
CC TO A LESSER EXTEND HOMODIMERS.
CC -1- ALTERNATIVE PRODUCTS:
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CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC IsoId=P07589-1; Sequence=Displayed;
CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
CC BY HEPATOCYTES, CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC -1- SIMILARITY: Contains 15 fibronectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00800; AAA0521.2; -.
CC PIR; A26452; FNBO.
CC HSSP; P02751; 2FN2.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR000083; Fibnrcnl.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR000562; FN Type II.
CC InterPro; IPR003962; FnIII_subd.
CC Pfam; PR00039; fnl; 12.
CC Pfam; PR00040; fn2; 2.
CC Pfam; PR00041; fn3; 15.
CC PRINTS; PR00013; FNTYPEII.
CC PRINTS; PR00014; FNTYPEIII.
CC ProDom; PD000995; FN Type II; 2.
CC SMART; SM00058; FN1_12.
CC SMART; SM00059; FN2; 2.
CC SMART; SM00060; FN3; 14.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS00023; FIBRONECTIN_2; 2.
CC PROSITE; PS01253; FIBRONECTIN_1; 12.
CC Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
CC Sulfation; Cell adhesion; Repeat; Alternative splicing;
CC Pyroliidone carboxylic acid.
CC MOD_RES 1 1
CC DOMAIN 21 241
CC FT 277 577
CC FT 876 1141
CC FT 1236 1509
CC FT 1600 1870
CC FT 1991 2216
CC FT 19 59
CC FT 64 107
CC FT 108 151
CC FT 153 197
CC FT 198 242
CC FT 275 314
CC FT 314 373
CC FT 374 438
CC FT 437 480
CC FT 485 527
CC FT 528 571
CC FT 578 669
CC FT 688 778
CC FT 779 874
CC FT 875 964
CC FT 965 1054
CC FT 1055 1141
CC FT 1142 1234
CC FT 1235 1325
CC FT 1326 1415
CC CELL-ATTACHMENT.
CC HEPARIN-BINDING. 2.
CC FIBRIN-BINDING 2.
CC FIBRONECTIN TYPE-I 1.
CC FIBRONECTIN TYPE-II 1.
CC FIBRONECTIN TYPE-III 1.
CC FIBRONECTIN TYPE-I 3.
CC FIBRONECTIN TYPE-I 4.
CC FIBRONECTIN TYPE-I 5.
CC FIBRONECTIN TYPE-I 6.
CC FIBRONECTIN TYPE-II 1.
CC FIBRONECTIN TYPE-II 2.
CC FIBRONECTIN TYPE-III 1.
CC FIBRONECTIN TYPE-III 2.
CC FIBRONECTIN TYPE-III 3.
CC FIBRONECTIN TYPE-III 4.
CC FIBRONECTIN TYPE-III 5.
CC FIBRONECTIN TYPE-III 6.
CC FIBRONECTIN TYPE-III 7.
CC FIBRONECTIN TYPE-III 8.
CC FIBRONECTIN TYPE-III 9.
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Query Match	Best Local Similarity	Score	DB 1	Length	2265
Matches 327; Conservative	96.3%;	1927;	DB 1;	Length 2265;	
	96.5%;	Pred. No. 2.5e-151;			
	6;	Mismatches 6;	Indels 0;	Gaps 0	
Qy 3	AVYQGPHPQPPPHGCHVTDSGVVSVGMQMLKTGQNKMLCTCLANGVSCQETAVTQTY	62			
Db 261	AIYQGPHPQPPPHGCHVTDSGVVSVGMQMLKTGQNKMLCTCLANGVSCQETAVTQTY	320			
Qy 63	GGNSGGEPCVLPEFTNGRFRFVSCTEGRDDGLMGSSTSNVYBODQKYSFCTDHTVLYVQR	122			
Db 321	GGNSGGEPCVLPEFTNGKTFKFSCTTEGRDDGHLMGSSTSNVYBODQKYSFCTDHTVLYVQR	380			
Qy 123	GGNSGALCHPEFLVNNHNYTCTSEGRDNNKWCCTTQNYADQKFGCPMAAHEICT	182			
Db 381	GGNSGALCHPEFLVNNHNYTCTSEGRDNNKWCCTTQNYADQKFGCPMAAHEICT	440			
Qy 183	TNEGVMYRIGDQWDKQHDGMHMRCTCVANGSGEWTCLAVSGLRDCIIVDITVYVNTFF	242			

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Db      441.  TNEGVMYR.I.GDQWDKQHDHGMHNRCTCYGNRKGEMTCVASYQLDQCIIVGITYNVNPDF 560
QY      243  HKHEBEGHMLNCTCFQGGGRMKCDPVDQCCDSEFTGFYQIGDSMEKYVHGCRYCYG 3020
Db      501  HKHEBEGHMLNCTCFQGGGRMKCDPVDQCCDSEFTGFYQIGDSMEKYQLGVRYQCYG 5600
QY      303  RGI.GEMHCDPLQTPYSSGSPVVFPTTEPSSQNSHP10M 341
Db      561  RGI.GEMACDPLQTPDTSQPVVQVITTEPSSQNSHP10M 599

RESULT 3
FINC_RAT
ID      FINC_RAT      STANDARD;      PRT;      2477 AA.
AC      P04937;
DT      13-AUG-1987 (Rel. 05, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Fibronectin precursor (FN).
GN      FN1.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Fischer; TISSUE=liver;
RX      MEDLINE=88054951; PubMed=2445560;
RA      Schwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;
RT      "Multiple sites of alternative splicing of the rat fibronectin gene
RL      transcript.";
RL      EMBO J. 6:2573-2580 (1987).
RN      [2]
RP      SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.
RC      STRAIN=Fischer; TISSUE=liver;
RX      MEDLINE=88054950; PubMed=3119333;
RA      Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.;
RT      "Organization of the fibronectin gene provides evidence for exon
RL      shuffling during evolution.";
RL      EMBO J. 6:2565-2572 (1987).
RN      [3]
RP      SEQUENCE OF 1586-2477 FROM N.A.
RX      MEDLINE=84082067; PubMed=6317187;
RA      Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.;
RT      "Three different fibronectin mRNAs arise by alternative splicing
RL      within the coding region.";
RL      Cell 35:421-431 (1983).
CC      -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
CC      INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
CC      ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
CC      HEALING, AND MAINTENANCE OF CELL SHAPE.
CC      -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC      VARIANTS. CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC      TO A LESSER EXTEND HOMODIMERS.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=4;
CC      Comment=Each of the "extra domain" and the connecting strand 3
CC      are present in some forms of fibronectin and absent in others;
CC      Name=1;
CC      IsoId=P04937-1; Sequence=Displayed;
CC      Name=2; Synonyms=FNII-13-less;
CC      IsoId=P04937-2; Sequence=VSP_003258;
CC      Name=3; Synonyms=lambda-RLP4-5;
CC      IsoId=P04937-3; Sequence=VSP_003259;
CC      Name=4; Synonyms=lambda-RLP6;
CC      IsoId=P04937-4; Sequence=VSP_003260;
CC      -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
CC      BY HEPATOCYTES, CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
CC      FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
CC      DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX.
CC      -1- PTM: SULFATED (BY SIMILARITY).
CC      -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC      -1- SIMILARITY: Contains 2 fibronectin type II domains.

```

CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; X15906; CA34020.1; -;
 DR EMBL; L29191; AAA41166.1; -;
 DR EMBL; L29191; AAA41166.1; JOINED.
 DR EMBL; L29191; AAA41167.1; -;
 DR EMBL; L29191; AAA41167.1; JOINED.
 DR EMBL; L29191; AAA41168.1; -;
 DR EMBL; L29191; AAA41168.1; JOINED.
 DR EMBL; X05831; CAA29278.1; -;
 DR EMBL; X05831; CAA29278.1; -;
 DR EMBL; X05833; CAA29280.1; -;
 DR EMBL; X05834; CAA29281.1; -;
 DR EMBL; X05834; CAA29281.1; -;
 DR HSP; S14428; S14428.
 DR HSP; P02751; 1PBR.
 DR InterPro; IPRO06209; EGF-like.
 DR InterPro; IPRO00083; Fibronctn.
 DR InterPro; IPRO03961; FN III.
 DR InterPro; IPRO00562; FN_type_II.
 DR InterPro; IPRO03962; FNIII_sdbd.
 DR Pfam; PF00039; fn1; 12.
 DR Pfam; PF00040; fn2; 2.
 DR Pfam; PF00041; fn3; 17.
 DR PRINTS; PR00013; FNTPR1.
 DR PRINTS; PR00014; FNTPR1.
 DR ProDom; PD000995; FN_Type_II; 2.
 DR SMART; SM00058; FN1; 12.
 DR SMART; SM00059; FN2; 2.
 DR SMART; SM00060; FN3; 13.
 DR PROSITE; PS00023; EGF_1; 2.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 DR GlycoProfile; Plasma; Heparin-binding; Acute phase; Phosphorylation;
 KW Sulfation; Cell adhesion; Repeat; Alternative splicing; Signal.
 FT FT CHAIN 1 32
 FT FT SIGNAL 33 2477
 FT FT DOMAIN 53 273
 FT FT DNAS_BIND 308 608
 FT FT DOMAIN 906 1171
 FT FT DOMAIN 1357 1630
 FT FT DOMAIN 1811 2081
 FT FT DOMAIN 2296 2427
 FT FT DOMAIN 51 91
 FT FT DOMAIN 96 139
 FT FT DOMAIN 140 183
 FT FT DOMAIN 185 229
 FT FT DOMAIN 230 274
 FT FT DOMAIN 345 306
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 FT FT DOMAIN 468 511
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 FT FT DOMAIN 707 808
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 FT DISULFID 232 261
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 FT CARBOHYD 542 542
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 FT CARBOHYD 1006 1006
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 FT CARBOHYD 2198 2198
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 FT VARSPLIC 1720 1809
 FT VARSPLIC 2082 2106
 FT VARSPLIC 2082 2200
 FT CONFLICT 2318 2318
 FT SEQUENCE 2477 AA; 272510 MM; B4391A47ECDEB5 CRC64;
 SQ
 Query Match 93.8%; Score 1877; DB 1; Length 2477;
 Best Local Similarity 93.2%; Pred. No. 3.7e-147;
 Matches 316; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 QY 3 AAYQPPHPQPPYGHCVTDGVSVMQMLTKGQNKQMLCTCLANGVSCQETAVTQY 62
 DB 292 AAYQPPHPQPPYGHCVTDGVSVMQMLTKGQNKQMLCTCLANGVSCQETAVTQY 351
 QY 63 GGSNSBPCTLPPTNNGRTFYSCCTTGRODGHMCSTSNYEDQKXSFETDITVYQTR 122
 DB 352 GGSNSBPCTLPPTNNGRTFYSCCTTGRODGHMCSTSNYEDQKXSFETDITVYQTR 411
 QY 123 GGSNGALGHFPLVNNHYTDTSEGRDNMKMCGTTONYVDADQKFGCPMAAHEICT 182

Db 412 GGNNGALCHPEFLYSNBNYSDCTSEGRDMMKACGTTQNTDADOKEGFCMAAHEICT 471
Qy 183 TNEGVWRIQDQMDKQDHMGHMECTCVNGRGWTCIAYSQLRDOCIYDDITVNVNDF 242
Db 472 TNEGVWRIQDQMDKQDHMGHMECTCVNGRGWTCIAYSQLRDOCIYDDITVNVNDF 531
Qy 243 HKRHEEGHMLNCTGCGGGRGWKCDPVNQCDDSEGTGTYYQIGDSMEKXVHGVRRQCYG 302
Db 532 HKRHEEGHMLNCTGCGGGRGWKCDPIDRCDDSEGTGTYYQIGDSMEKXVHGVRRQCYG 591
Qy 303 RGIGEMHCQPLQTPSSSGPVEVFTTEPSPQNSHPQM 341
Db 592 RGIGEMHCQPLQTPGTTGPVQVITTEPSPQNSHPQM 630

RESULT 4
FINC_XENLA STANDARD: PRT: 2481 AA.
ID_FINC_XENLA
AC Q91740;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibronectin precursor.
GN FN1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OX Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92111942; PubMed=1730390;
RA Desimone D.W., Norton P.A., Hynes R.O.;
RT "Identification and characterization of alternatively spliced
RT fibronectin mRNAs expressed in early Xenopus embryos.";
RL Dev. Biol. 149:357-369(1992).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
CC HEALING, AND MAINTENANCE OF CELL SHAPE (BY SIMILARITY).
CC -1- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
CC CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
CC SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC IsoId=Q91740-1; Sequence=Displayed; EMBRYO, CELLULAR FORMS OF
CC -1- TISSUE SPECIFICITY: IN EARLY XENOPUS EMBRYO, CELLULAR FORMS OF
CC FIBRONECTIN PREDOMINATE WHICH INCLUDE BOTH EXTRA DOMAIN. IN
CC FIBRONECTIN OF EMBRYONIC AND ADULT LIVER THE CONNECTING STRAND 3
CC CAN BE EITHER COMPLETELY EXCLUDED OR INCLUDED.
CC -1- SIMILARITY: Contains 12 fibronectin type II domains.
CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M77820; AAA49707.1; -
DR HSSP; P02751; 2FN2.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibnctn1.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; Fn1; 12.

DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00013; FNTYPEII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 17.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 11.
KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
KW Repeat; Alternative splicing; Signal.
FT SIGNAL 1 31
FT CHAIN 32 2481
FT DOMAIN 55 275
FT DOMAIN 309 609
FT DNA_BIND 907 1172
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FT DOMAIN 53 93
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FT FIBRONECTIN.
FT FIBRIN- AND HEPARIN-BINDING 1.
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FT BY SIMILARITY.
FT CELL-ATTACHMENT.
FT HEPARIN-BINDING 2.
FT FIBRIN-BINDING 2.
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FT DISULFID 2301 2330 BY SIMILARITY.
 FT DISULFID 2328 2340 BY SIMILARITY.
 FT DISULFID 2346 2373 BY SIMILARITY.
 FT DISULFID 2371 2383 BY SIMILARITY.
 FT DISULFID 2390 2414 BY SIMILARITY.
 FT DISULFID 2412 2428 BY SIMILARITY.
 FT DISULFID 2459 2459 INTERCHAIN (WITH 2463 OF OTHER CHAIN)
 FT DISULFID 2463 2463 (BY SIMILARITY).
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 529 529 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 543 543 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 877 877 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1244 1244 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1291 1291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2202 2202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 2481 AA; 272678 MW; 7E47DF4F6CE72C93 CRC64;

Query Match 79.5%; Score 1591; DB 1; Length 2481;
 Best Local Similarity 77.6%; Pred. No. 1,6e-123;
 Matches 263; Conservative 41; Mismatches 33; Indels 2; Gaps 1;

QY 3 AVYQPPHPPPPYHGVTVDSGVVYVGMQLTQGNKQMLCTCLANGVSCQETAVTQTY 62
 DB 295 ALVQPD--SGLBPGHCVTDNGVLVYLGKRWLTQSGKQMLCTCLANGVSCQETAVTTF 352
 QY 63 GGNNSNEPCVLTPTNGRTYSCCTBGRQNGHLMCTSTSYEDQKXSFCTDHTLVQTR 122
 DB 353 GGNANBEPCKAIPETHQKTYSCCTBGRQNGKLMCAITNSYDCKYSCFTEQALAVQTR 412
 QY 123 GGNNGALCHFPFLYNNHNTDCTSEGRDNMKCGTQNYDADOKFGCPMAAHEICT 182
 DB 413 GGNNGALCNFPFLYNNHNTDCTSEGRDMSKMGCTTANYDADOKFGCPMAAHEICT 472
 QY 183 TNEGVRIGDQDKOHDMGMKCTCVNGRGEWTCIAYSQURDQCIYDITVNVNDF 242
 DB 473 TNEGVMYRVGDQDKOHDMGMKCTCVNGRGEWTCIAYSQURDQCIYDITVNVNDF 532
 QY 243 HKHBEHGLNCTCFQGRGRMKCDPVDQCDSETGTFYQIGSWKTYHGVYQCYG 302
 DB 533 TKLBEHGMNCTCFQGRGRMKCDALDQCDSETGTFYQIGSWKTYHGVYQCYG 592
 QY 303 RGIGEMHCOPLQTPSSGPEVEFTETPSQNSHPLOW 341
 DB 593 KGIGEMHCOPLSTSQAGTGPVYITBSANFPTSHPIOW 631

RESULT 5

FINC NOTVI STANDARD; PRT; 190 AA.

AC Q91400;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Fibronectin (Fragment).
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Notophthalmus.
 NCBI_TaxID=8316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95252528; PubMed=7734733;
 RA Nace J.D., Tassava R.A.;
 RT Examination of fibronectin distribution and its sources in the
 RT regeneration newt limb by immunocytochemistry and in situ
 RT hybridization.";
 RL Dev. Dyn. 202:153-164(1995).
 CC -!- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
 CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
 CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
 CC HEALING, AND MAINTENANCE OF CELL SHAPE (BY SIMILARITY).

CC -!- FUNCTION: BENEATH WOUND EPITHELIUM, FIBRONECTIN PROBABLY PROVIDES
 CC A SUBSTRATE ON WHICH THE DIFFERENTIATION STUMP TISSUE CELLS WILL
 CC MIGRATE AND ACCUMULATE.
 CC -!- SUBUNIT: DIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANTS,
 CC CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: Contains at least 3 fibronectin type I domains.
 CC -!- SIMILARITY: Contains at least 1 fibronectin type II domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).

DR EMBL/ S76886; AAB34250.1; -
 DR PIR; I51279; I51279.
 DR HSSP; P02751; 2FN2.
 DR InterPro; IPR000083; Fibronctn1.
 DR InterPro; IPR000562; FN_Type_II.
 DR Pfam; PF00039; Fn1; 3.
 DR Pfam; PF00040; Fn2; 1.
 DR PRINTS; PR00013; FNYPEII.
 DR ProDom; PD000995; FN_Type_II; 1.
 DR SMART; SM00058; FN1; 3.
 DR SMART; SM00059; FN2; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
 KW Repeat.
 FT NON TER 1 1
 FT DOMAIN <1 98
 FT DOMAIN 55 56
 FT DOMAIN 103 145
 FT DOMAIN 146 >190
 FT DISULFID 57 85
 FT DISULFID 83 95
 FT DISULFID 105 132
 FT DISULFID 130 142
 FT CARBOHYD 17 17
 FT CARBOHYD 115 115
 FT CARBOHYD 129 129
 FT NON TER 190 190
 SQ SEQUENCE 190 AA; 21960 MW; 2C2033226DB4233 CRC64;

Query Match 48.0%; Score 961; DB 1; Length 190;
 Best Local Similarity 85.8%; Pred. No. 1,1e-72;
 Matches 163; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 125 NSNGALCHFPFLYNNHNTDCTSEGRDNMKCGTQNDADOKFGCPMAAHEICTTN 184
 DB 1 NSNGALCHFPFLYNNHNTDCTSEGRDMSKMGCTTANYDADOKFGCPMAAHEICTTN 60
 QY 185 EGVMYRIGDQDKOHDMGMKCTCVNGRGEWTCIAYSQURDQCIYDITVNVNDFPK 244
 DB 61 EGVMYRVGVGDQDKOHDMGMKCTCVNGRGEWTCIAYSQURDQCIYDITVNVNDFPK 120
 QY 245 RHEBGMNCTCFQGRGRMKCDPVDQCDSETGTFYQIGSWKTYHGVYQCYG 304
 DB 121 RHEBGMNCTCFQGRGRMKCDALDQCDSETGTFYQIGSWKTYHGVYQCYG 180
 QY 305 IGEWHCOPLQ 314
 DB 181 IGEWHCOPLQ 190

RESULT 6

MM09_RABIT STANDARD; PRT; 707 AA.

ID MM09_RABIT
 AC P41246;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB).
 GN MMP9.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 ON NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Japanese white; TISSUE=Bone;
 RX MEDLINE=94253056; Pubmed=8195136;
 RA Tezuka K.I., Nemoto K., Tezuka Y., Sato T., Ikeda Y., Kobori M.,
 RA Kawashima H., Eguchi H., Hakeda Y., Kumegawa M.;
 RT "Identification of matrix metalloproteinase 9 in rabbit osteoclasts";
 RL J. Biol. Chem. 269:15006-15009 (1994).
 RN [2]
 RP SEQUENCE OF 1-171 FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Liver;
 RX MEDLINE=95050662; Pubmed=7961810;
 RA Fitt M.E., Bartlett J.D., Matsubara M., Rinehart W.B., Mody M.K.,
 RA Girard M.T., Rainville M.;
 RT "The rabbit gene for 92-kDa matrix metalloproteinase. Role of API and
 AP2 in cell type-specific transcription.";
 RL J. Biol. Chem. 269:28620-28628 (1994).
 CC -1- FUNCTION: COULD PLAY A ROLE IN BONE OSTEOCLASTIC RESORPTION.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -1- TISSUE SPECIFICITY: OSTEOCLASTS.
 CC -1- SIMILARITY: THE CENTRAL DOMAIN SHOWS SIMILARITY TO THE TYPE-II
 CC MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN
 CC BINDS GELATIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D26514; BAA05520.1; -;
 DR EMBL; L36050; AAA64358.1; -;
 DR PIR; A53796; A53796.
 DR HSSP; P08254; 1COR.
 DR MEROPS; M10.004; -;
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrxin.
 DR InterPro; IPR006026; Nzn_Mtpeptidase.
 DR InterPro; IPR006970; PT.
 DR InterPro; IPR006025; Zn_Mtpeptidase.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00443; peptidase_M10; 1.
 DR Pfam; PF03933; peptidase_M10_N; 1.
 DR Pfam; PF04886; PT; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRXIN.
 DR PRODOM; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZmC; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 KW Hydrolase; Metalloproteinase; Glycoprotein; Zinc; Zymogen; Calcium;

KW Collagen degradation; Extracellular matrix; Repeat; Signal.
 FT SIGNAL 1
 FT PROPEP 20
 FT CHAIN 107
 FT DOMAIN 107
 FT DOMAIN 223
 FT DOMAIN 281
 FT DOMAIN 340
 FT DOMAIN 397
 FT SITE 513
 FT SITE 99
 FT METAL 401
 FT ACT SITE 402
 FT METAL 405
 FT METAL 411
 FT CARBOHYD 88
 FT CARBOHYD 120
 FT CARBOHYD 127
 FT DISULFID 516
 FT CONFLICT 76
 FT CONFLICT 100
 SQ SEQUENCE 707 AA; 78307 MW; 053BCE8DC4D4758F CRC64;
 Query Match 19.8%; Score 396.5; DB 1; Length 707;
 Best Local Similarity 45.4%; Pred. No. 2.2e-25;
 Matches 79; Conservative 23; Mismatches 49; Indels 23; Gaps 6;
 Oy 16 YGHCVTDSGVVSYVMQMLKTQGNKQMLCTCLGNGVSCQETAVLYQTYGNSNGEPVLPF 75
 Db 241 YTACTTDG---RSDGMWMCSTTADYD---TDRRGFGPSESLYIQ--DGNADGKPCPEPF 292
 Oy 76 TYNARTYSCCTBEROGHLMCTSTNYEDQKSF---TDHIVLYQTRGNSNGALCH 132
 Db 293 IFQGRYSACTDGRSDGHRWCATYADKDLGFPETRADSTIV---GNSAGEICLV 348
 Oy 133 PPFLYNNHNTDCTSEGRPDNMKWCCTONYADQKGFPC-----MAAHE 178
 Db 349 PPFVFLGKRYSSCTSEGRDRLMCATITSNFSDKMKWFCPDKYSFLVAABE 402
 RESULT 7
 MM02_RABIT STANDARD; PRT; 662 AA.
 AC P50757;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
 DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
 GN MMP2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 ON NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Japanese white; TISSUE=Articular joint;
 RX MEDLINE=96283805; Pubmed=8679695;
 RA Matsunoto S., Katoh M., Matanabe T., Masuh Y.;
 RT "Molecular cloning of rabbit matrix metalloproteinase-2 and its broad
 RT expression at several tissues";
 RL Biochim. Biophys. Acta 1307:137-139 (1996).
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
 CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-gln-gly-|-
 CC Ile-Ala-gly-Gln.
 CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
 CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
 CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
 CC MMP3) (By similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL; D63579; BAA09796.1; -
 DR PIR; S70365; S70365.
 DR HSSP; P08253; 1RTG.
 DR MEROPS; M10.003; -
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrixin.
 DR InterPro; IPR006026; Nzn_MTPeptide.
 DR InterPro; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRIXIN.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMC; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR HydroLase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 KM Collagen degradation; Extracellular matrix; Repeat; Signal.
 FT SIGNAL; 1 29
 FT PROPEP; 30 109
 FT CHAIN; 110 662
 FT DOMAIN; 110 221
 FT DOMAIN; 222 396
 FT DOMAIN; 397 467
 FT DOMAIN; 226 283
 FT DOMAIN; 284 341
 FT DOMAIN; 342 399
 FT DOMAIN; 468 662
 FT SITE; 102 102
 FT METAL; 403 403
 FT METAL; 404 404
 FT ACT_SITE; 407 407
 FT METAL; 413 413
 FT CARBOHYD; 575 575
 FT CARBOHYD; 644 644
 FT DISULFID; 471 662
 SQ SEQUENCE 662 AA; 73803 MW; 1CC246B270E440C8 CRC64;

Query Match 19.3%; Score 386.5; DB 1; Length 662;
 Best Local Similarity 38.8%; Pred. No. 1.4e-24;
 Matches 80; Conservative 29; Mismatches 76; Indels 21; Gaps 6;

QY 55 ETAVTQYGGNSNSPEPCVLPFTVNGKRFYSCCTEGRDDGHMCSTGNYEQDQXSCSTD 114
 DB 217 EGVAVRYKYNADEYKFPFLFNGKEYTSCSTDGRSDGFLWCSTYTNFEDGKGYFC-P 275
 QY 115 HTVLVVRGNSNSALCHPPLLYNNHYTDCSTSEGRDNMKMCGTTONYADQKFGFCPM 174
 DB 276 HEALF-TMGSNADQPKCFPRFRGCTSYSSCTTGKRDGKRWCTTDYDRDKKYGKCP 334
 QY 175 AAHEICTTNGV-----MYRIGQMDKQDHMGHMCCTCVNGRGEMTCTIA---YSQLR 226
 DB 335 TANGSTIGNSGAPCVFPFTFLGKYES-----CTSGRSDGKMWCTSTNYDDDR 385
 QY 227 DQCTIVDITNVNNTFKRHEGHL 252
 DB 386 KWGFCPDQGYSL--FLVAHHEFGHAM 409

RESULT 8

MM02 MOUSE
 ID MM02 MOUSE STANDARD; PRT; 662 AA.
 AC P3434;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
 DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
 GN MMP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2218452; PubMed=1373140;
 RA Reponen P., Sahberg C., Huhtala P., Hurskainen T., Theisfeldt I.,
 RA Tytgavaen K.;
 RT "Molecular cloning of murine 72-kDa type IV collagenase and its
 RT expression during mouse development.";
 RL J. Biol. Chem. 267:7856-7862(1992).
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
 CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-Ile-
 CC Ile-Ala-Gly-Gln.
 CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
 CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
 CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
 CC MMP3) (by similarity).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
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 CC or send an email to license@isb-sib.ch).

DR EMBL; M64324; AAA39338.1; -
 DR PIR; A42496; A42496.
 DR HSSP; P08253; 1RTG.
 DR MEROPS; M10.003; -
 DR MCD; MGT.97009; MMP2.
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrixin.
 DR InterPro; IPR006026; Nzn_MTPeptide.
 DR InterPro; IPR006025; Zn_MTPeptide.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRIXIN.
 DR ProDom; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMC; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR HydroLase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 KM Collagen degradation; Extracellular matrix; Repeat; Signal.
 FT SIGNAL; 1 29
 FT PROPEP; 30 109
 FT CHAIN; 110 662
 FT DOMAIN; 110 221
 FT DOMAIN; 222 396
 FT DOMAIN; 397 467
 FT DOMAIN; 226 283

```

FT DOMAIN 284 341 FIBRONECTIN TYPE-II 2.
FT DOMAIN 342 399 FIBRONECTIN TYPE-II 3.
FT DOMAIN 468 662 HEMOPEXIN-LIKE.
FT SITE 102 102 CYSTEINE SWITCH (POTENTIAL).
FT METAL 403 403 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 404 404 BY SIMILARITY.
FT METAL 407 407 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 413 413 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 575 575 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 471 662 BY SIMILARITY.
SQ SEQUENCE 662 AA; 74102 MW; C630A7DBDB272F02 CRC64;

Query Match 19.3%; Score 385.5; DB 1; Length 662;
Best Local Similarity 38.8%; Pred. No. 1.6e-24;
Matches 80; Conservative 28; Mismatches 77; Indels 21; Gaps 6;

Qy 55 ETAVTQYVGNNSGNCPLPTVNGRTFYSCCTEGROGHLMGCTSYVEDOKYSFCTD 114
Db 217 EGQVVRVRYGNADGECYCFPLFNREYSSCTDGRSDGFLMCSITVNFEXKGYGFC-P 275
Qy 115 HTVAVOTRGNSNGALCHFPFLYNNHNYTDCTSEGRDNMKCGTTONYDADOKFGCPM 174
Db 276 HEALF-TMGSNADGQPCFPFRFGTSTNSCTTBERTGYRWCCTTEDYDRDKXGFCPE 334
Qy 175 AAHEICTTNEG- ----MYRIGDQWKDQHDGMHMRCTCVGNRGGEWTCIA---YSQLR 226
Db 335 TAMSTVGNSESGAPCVFPFTFLGNKYES- ----CTSGRNDGKVCATTTNYDDDR 385
Qy 227 DQCIYDITVNVNDFPHGRHEGHL 252
Db 386 KWGFCPDGYSL-FLVAHEFGHAM 409

RESULT 9
MM02_RAT STANDARD; PRT; 662 AA.
ID _MM02_RAT STANDARD; PRT; 662 AA.
AC P33436; P97581;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
GN gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBT_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93249363; PubMed=7916617;
RA Marti H.P., McNeill L., Davies M., Martin J., Lovett D.H.;
RT "Homolog cloning of rat 72 kDa type IV collagenase: cyckline and
RT second-messenger inducibility in glomerular mesangial cells.";
RL Biochem. J. 291:441-446(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Mistar; TISSUE=skin;
RA Okada A., Basset P.;
RT "The cloning of the cDNA encoding rat gelatinase A from a rat skin
RT wound cDNA library.";
RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-I-
CC Ile-Ala-Gly-Gln.
CC -1- COPACITOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
CC -1- PFM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
CC MMP3) (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -1- SIMILARITY: Contains 3 fibronectin type II domains.

```

```

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CC or send an email to license@isb.ch).
CC -----
CC EMBL; X71466; CA50583.1; -
CC EMBL; U65656; AAB41692.1; -
CC PIR; S34780; S34780.
CC HSSD; P08253; IRTG.
CC MEROPS; M10.003; -.
CC InterPro; IPR000562; FN_Type_II.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Matrixin.
CC InterPro; IPR006026; Zn_MTPeptide.
CC InterPro; IPR006025; Zn_MTPeptide.
CC Pfam; PF00040; fn2; 3.
CC Pfam; PF00045; hemopexin; 4.
CC Pfam; PF00413; peptidase_M10; 1.
CC Pfam; PF03933; peptidase_M10_N; 1.
CC PRINTS; PR00013; FMYPRIT.
CC PRINTS; PR00138; MATRIXIN.
CC ProDom; PD00095; FN_Type_II; 3.
CC SMART; SM00059; FN2; 3.
CC SMART; SM00120; HX; 4.
CC SMART; SM00235; Zmc; 1.
CC PROSITE; PS00023; FIBRONECTIN_2; 3.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
CC KX Hydroxylase; Metalloproteinase; Glycoprotein; Zinc; Zymogen; Calcium;
CC Collagen degradation; Extracellular matrix; Repeat; Signal.
CC FT SIGNAL 1 29
CC FT PROPEP 30 109
CC FT CHAIN 110 662
CC FT DOMAIN 110 221
CC FT DOMAIN 222 396
CC FT DOMAIN 397 467
CC FT DOMAIN 467 662
CC FT DOMAIN 284 341
CC FT DOMAIN 342 399
CC FT DOMAIN 468 662
CC FT METAL 102 102
CC FT METAL 403 403
CC FT ACT_SITE 404 404
CC FT METAL 407 407
CC FT METAL 413 413
CC FT CARBOHYD 575 575
CC FT CARBOHYD 644 644
CC FT DISULFID 471 662
CC FT CONFLICT 42 42
CC FT CONFLICT 286 286
CC FT CONFLICT 369 369
CC FT CONFLICT 435 435
CC FT CONFLICT 586 586
CC SQ SEQUENCE 662 AA; 74181 MW; 7496B34B0A21884B CRC64;

Query Match 19.3%; Score 385.5; DB 1; Length 662;
Best Local Similarity 38.8%; Pred. No. 1.6e-24;
Matches 80; Conservative 28; Mismatches 77; Indels 21; Gaps 6;

Qy 55 ETAVTQYVGNNSGNCPLPTVNGRTFYSCCTEGROGHLMGCTSYVEDOKYSFCTD 114
Db 217 EGQVVRVRYGNADGECYCFPLFNREYSSCTDGRSDGFLMCSITVNFEXKGYGFC-P 275
Qy 115 HTVAVOTRGNSNGALCHFPFLYNNHNYTDCTSEGRDNMKCGTTONYDADOKFGCPM 174
Db 276 HEALF-TMGSNADGQPCFPFRFGTSTNSCTTBERTGYRWCCTTEDYDRDKXGFCPE 334
Qy 175 AAHEICTTNEG- ----MYRIGDQWKDQHDGMHMRCTCVGNRGGEWTCIA---YSQLR 226

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DB 335 TAWSTVGNSEGAFCVFPFLFNKYES-----CTSGNRNDKWCATTTNVDDB 385
 QY 227 DQCIYDITVNVNDTFHKEBGMHL 252
 DB 386 KMGFCPPDQISTL--FLVAAREFHGM 409

RESULT 10
 ID MM02_HUMAN STANDARD; PRT; 660 AA.
 AC P08253;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 72 kDa type IV collagenase precursor (BC 3.4.24.24) (72 kDa
 gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A)
 DE (TBE-1).
 GN MMP2 OR CLG4A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBL TaxID=9606;
 RN [1]
 RP SEQUENCE OF 19-660 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88198218; PubMed=2834383;
 RA Collier I.E., Wilhelm S.M., Eisen A.Z., Marmer B.L., Grant G.A.,
 RA Selster J.L., Kronenberg A., He C., Bauer E.A., Goldberg G.I.,
 RA "H-ras oncogene-transformed human bronchial epithelial cells (TBE-1)
 RT secrete a single metalloproteinase capable of degrading basement
 RT membrane collagen".
 RL J. Biol. Chem. 263:6579-6587(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91236162; PubMed=1851724;
 RA Collier I.E., Burns G.A.P., Goldberg G.I., Gerhard D.S.,
 RT "On the structure and chromosome location of the 72- and 92-kDa human
 RT type IV collagenase genes".
 RL Genomics 9:429-434(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90293047; PubMed=2162831;
 RA Huhtala P., Chow L.T., Trygvaason K.,
 RT "Structure of the human type IV collagenase gene".
 RL J. Biol. Chem. 265:11077-11082(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
 RA Spatler M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toibinuk S., Cannici P., Prange C.,
 RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallin D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-51 FROM N.A.
 RX MEDLINE=90228972; PubMed=2158484;
 RA Huhtala P., Eddy R.L., Fan Y.S., Byers M.G., Shows T.B.,
 RA Trygvaason K.,

RT "Completion of the primary structure of the human type IV collagenase
 RT preproenzyme and assignment of the gene (CLG4) to the q21 region of
 RT chromosome 16".
 RL Genomics 6:554-559(1990).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 443-660.
 RX MEDLINE=96069777; PubMed=758364;
 RA Libson A.M., Gittis A.G., Collier I.E., Marmer B.L., Goldberg G.I.,
 RA Lattman E.E.,
 RT "Crystal structure of the haemopexin-like C-terminal domain of
 RT gelatinase A".
 RL Nat. Struct. Biol. 2:938-942(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 458-660.
 RX MEDLINE=96140723; PubMed=8549817;
 RA Golike U., Gomis-Ruth F.X., Crabbe T., Murphy G., Docherty A.J.,
 RA Bode W.,
 RT "The C-terminal (haemopexin-like) domain structure of human
 RT gelatinase A (MMP2): structural implications for its function".
 RL FEBS Lett. 378:126-130(1996).
 CC -1- CATALYTIC ACTIVITY: cleavage of gelatin type I and collagen types
 CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-
 CC Ile-Ala-Gly-Gln.
 CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
 CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY NORMAL SKIN FIBROBLASTS.
 CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
 CC MMP3).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
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 CC -----
 DR EMBL J03210; AAA35701.1; -
 DR EMBL M33789; AAA52027.1; -
 DR EMBL M55593; AAA52028.1; -
 DR EMBL M58552; AAA52028.1; JOINED.
 DR EMBL M55582; AAA52028.1; JOINED.
 DR EMBL M55583; AAA52028.1; JOINED.
 DR EMBL M55584; AAA52028.1; JOINED.
 DR EMBL M55585; AAA52028.1; JOINED.
 DR EMBL M55586; AAA52028.1; JOINED.
 DR EMBL M55587; AAA52028.1; JOINED.
 DR EMBL M55588; AAA52028.1; JOINED.
 DR EMBL M55589; AAA52028.1; JOINED.
 DR EMBL M55590; AAA52028.1; JOINED.
 DR EMBL M55591; AAA52028.1; JOINED.
 DR EMBL M55592; AAA52028.1; JOINED.
 DR EMBL BC002576; AAH02576.1; -
 DR EMBL A28153; A28153.
 DR PDB 1RTG; 10-JUN-96.
 DR PDB 1GEN; 17-AUG-96.
 DR PDB 1CK7; 25-AUG-99.
 DR PDB 1CKW; 12-NOV-99.
 DR PDB 1HOV; 20-DEC-02.
 DR PDB 1J7M; 22-AUG-01.
 DR PDB 1K50; 17-APR-02.
 DR PDB 1QIB; 19-NOV-99.
 DR MEROPS; M10.003; -.
 DR Genew; HGNC:7166; MMP2.
 DR MTM; 120360; -
 DR GO; GO:000615; Extracellular space; TAS.
 DR GO; GO:000428; F:gelatinase A activity; TAS.
 DR GO; GO:0008270; F:zinc ion binding activity; TAS.
 DR InterPro; IPR000562; FN Type II.
 DR InterPro; IPR000585; Hemopexin.

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DR InterPro; IPR001818; Matrxin.
DR InterPro; IPR006026; Zn_MTPeptide.
DR InterPro; IPR006025; Zn_MTPeptide.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; peptidase_M10; 1.
DR PRINTS; PR00013; FNTPEPT.
DR PRINTS; PR00138; MATRXIN.
DR PRODOM; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZNMC; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 109 ACTIVATION PEPTIDE.
FT CHAIN 110 660 72 kDa type IV COLLAGENASE.
FT DOMAIN 110 221 COLLAGENASE-LIKE 1.
FT DOMAIN 222 396 COLLAGEN-BINDING.
FT DOMAIN 397 465 COLLAGENASE-LIKE 2.
FT DOMAIN 226 283 FIBRONECTIN TYPE-II 1.
FT DOMAIN 342 399 FIBRONECTIN TYPE-II 2.
FT DOMAIN 466 660 FIBRONECTIN TYPE-II 3.
FT DOMAIN 102 102 HEMOPEXIN-LIKE.
FT METAL 102 102 CYSTEINE SWITCH (POTENTIAL).
FT METAL 403 403 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 404 404 BY SIMILARITY.
FT METAL 407 407 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 413 413 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 573 573 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 469 660
FT TURN 468 470
FT STRAND 477 481
FT TURN 482 483
FT STRAND 484 489
FT TURN 490 491
FT STRAND 492 496
FT TURN 499 500
FT STRAND 504 508
FT HELIX 509 511
FT TURN 512 512
FT TURN 514 515
FT STRAND 522 526
FT TURN 527 530
FT STRAND 531 536
FT TURN 537 538
FT STRAND 539 544
FT TURN 545 546
FT STRAND 547 548
FT TURN 550 551
FT STRAND 554 555
FT HELIX 556 559
FT TURN 560 560
FT TURN 563 564
FT STRAND 570 574
FT TURN 575 578

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Query Match 19.1%; Score 382.5; DB 1; Length 660;
 Best Local Similarity 38.3%; Pred. No. 2.9e-24;
 Matches 79; Conservative 28; Mismatches 78; Indels 21; Gaps 6;

QY 55 ETAVTQTGYGNSNBPCLPTFYNGRTFYSCCTEGROGHLMCTSTSYEDODKYSFCTD 114
 Db 217 EGVGVRYKYGNADEYCKFPFLFNKKEYNSTCTDGRSGFLMCTSTTYFEKDGKYGFC-P 275
 QY 115 HTVLVQTRGNSNGALCHFPFLYNNHNYTDCSTSGRDRNMKWCCTTQNYDADOKFGFCFM 174

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Db 276 HEALF-TWGNVAEQPKFPFRFGTSTYDSCITTEGRDGYRWCCTTBDYDRKRYGCPCE 334
QY 175 AAHEICTNVEV-----MYRIGQMDKQDHMMAMCTGVNGRGWTGIA---YSQLR 226
Db 335 TAMSTVGNSRGACVCPFFFLGNKYES-----CTSGRSDGKMKWCATTANYDDDR 385
QY 227 DQCIYDDITVNVNDTFKRHEEGHML 252
Db 386 KWGFCPDQGYSL--FLVAHEFGHAM 409

RESULT 11
ID MM02_CHICK STANDARD; PRT; 663 AA.
AC 090611;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 72 kDa type IV collagenase precursor (EC 3.4.24.24) (72 kDa
DE gelatinase) (Matrix metalloproteinase-2) (MMP-2) (Gelatinase A).
GN MMP2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94280397; PubMed=8010954;
RA Aimes R.T., French D.L., Quigley J.P.;
RT "Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from
RT chicken embryo fibroblasts using gene family PCR: expression of the
RT gelatinase increases upon malignant transformation."
RL Biochem. J. 300:729-736(1994).
RN [2]
RP SEQUENCE OF 27-41 AND 107-122.
RX MEDLINE=91161603; PubMed=1848240;
RA Chen J.-M., Aimes R.T., Ward G.R., Youngleib G.L., Quigley J.P.;
RT "Isolation and characterization of a 70-kDa metalloproteinase
RT (gelatinase) that is elevated in Rous sarcoma virus-transformed
RT chicken embryo fibroblasts."
RL J. Biol. Chem. 266:5113-5121(1991).
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin type I and collagen types
CC IV, V, VII, X. Cleaves the collagen-like sequence Pro-Gln-Gly-|-
CC Ile-Ala-Gly-Gln.
CC -1- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -1- SUBUNIT: LIGAND FOR INTEGRIN ALPHA-V/BETA-3.
CC -1- TISSUE SPECIFICITY: PRODUCED BY NORMAL SKIN FIBROBLASTS.
CC -1- PTM: The propeptide is processed by MMP14 (MT-MMP1) and MMP16 (MT-
CC MMP3) (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M0A.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
CC -----
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DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; ENTPEPIT.
DR PRINTS; PR00138; MATRILXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZMNC; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolyase; Metalloprotease; Zinc; Zymogen; Calcium; Repeat;
KM Collagen degradation; Extracellular matrix; Signal.
FT SIGNAL 1 26
FT PROPP 27 106 ACTIVATION PEPTIDE.
FT CHAIN 107 663 72 kDa TYPE IV COLLAGENASE.
FT DOMAIN 107 218 COLLAGENASE-LIKE 1.
FT DOMAIN 219 393 COLLAGEN-BINDING.
FT DOMAIN 394 468 COLLAGENASE-LIKE 2.
FT DOMAIN 223 280 FIBRONECTIN TYPE-II 1.
FT DOMAIN 281 338 FIBRONECTIN TYPE-II 2.
FT DOMAIN 339 396 FIBRONECTIN TYPE-II 3.
FT DOMAIN 469 663 HEMOPEXIN-LIKE.
FT SITE 99 99 CYSTEINE SWITCH (POTENTIAL).
FT METAL 400 400 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 401 401 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 404 404 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 410 410 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISUFID 472 663 BY SIMILARITY.
FT CONFLICT 40 40 P -> Q (IN REF. 2).
FT CONFLICT 116 116 W -> T (IN REF. 2).
FT CONFLICT 122 122 T -> I (IN REF. 2).
SQ SEQUENCE 663 AA; 74941 MW; 8D6FDA867C3EBCA CRC64;

Query Match 19.1%; Score 382.5; DB 1; Length 663;
Best Local Similarity 37.0%; Pred. No. 2.9e-24;
Matches 77; Conservative 31; Mismatches 75; Indels 25; Gaps 6;

QY 55 ETAVTQTGGNSGPEVLPFTYNGRTFYSCTEGRDGHLMGCTSNVYEQDKYSFCTD 114
Db 214 EGVVAVKYNAGNAGVCKPFFWNGKYNCTDAGRNDGLMCTTDPADKRYGCPH 273
QY 115 HTLVVOTRGNSNGALCHPEPLVNNHNTDCTSEGRDNNKMGCTTQNYADQKFGFCPM 174
Db 274 ESIF--TMGNGDGOCPCKPFFKFGQSYDQCTTEGRDGYRWGCTEDYDRDKYGFCE 331
QY 175 AAHEBICITNEG------WRIGDQMDKHDMGHMRCCTCVNGRGRTGIAYSQLRDQ- 228
Db 332 TAMSTVGNSGSGAPCVPFPIFLNKKYDS-----CTAGRNDDGLMCASTSSYDDDR 382
QY 229 ----CIVDITVNVNDTFHRRHEGHML 252
Db 383 KMGFC--PDGYSL--FLVAHHRFGHAM 406

RESULT 12
MM09 RAT STANDARD; PRT; 708 AA.
ID MM09 RAT STANDARD; PRT; 708 AA.
AC PS0282;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN MMP9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=96184505; PubMed=8605986;
RA Xia Y., Garcia G., Chen S., Wilson C.B., Feng L.;
RT "Cloning of rat 92-kDa type IV collagenase and expression of an
RT active recombinant catalytic domain.";
RL FEBS Lett. 382:285-288(1996).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=96069602; PubMed=7590350;
RA Okada A., Santavica M., Bassett P.;
RT "The cdna cloning and expression of the gene encoding rat gelatinase
RT B."
RL Gene 164:317-321(1995).

CC -1- FUNCTION: COULD PLAY A ROLE IN BONE OSTEOCLASTIC RESORPTION.
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
CC types IV and V.
CC -1- COPACITOR: Binds 2 zinc ions per subunit, calcium (by similarity).
CC -1- SIMILARITY: THE CENTRAL DOMAIN SHOWS SIMILARITY TO THE TYPE-II
CC MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN
CC BINDS GELATIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
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CC or send an email to license@isb-sib.ch).
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DR EMBL; U36476; AA01721.1; -
DR EMBL; U24441; AA090911.1; -
DR PIR; JCA364; JCA364.
DR HSSP; P08254; IUSN.
DR MEROPS; M10.004; -
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrxin.
DR InterPro; IPR006026; NZn_Mtpetdase.
DR InterPro; IPR006970; PT.
DR InterPro; IPR006025; Zn_MTPetdase.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR Pfam; PF04886; PT; 1.
DR PRINTS; PR00013; ENTPEPIT.
DR PRINTS; PR00138; MATRILXIN.
DR ProDom; PD000995; FN_Type_II; 3.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZMNC; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
KW Hydrolyase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
KW Collagen degradation; Extracellular matrix; Repeat; Signal.
FT SIGNAL 1 19
FT PROPP 20 107 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 108 708 92 kDa TYPE IV COLLAGENASE.
FT DOMAIN 224 281 FIBRONECTIN TYPE-II 1.
FT DOMAIN 282 340 FIBRONECTIN TYPE-II 2.
FT DOMAIN 341 398 FIBRONECTIN TYPE-II 3.
FT DOMAIN 398 708 HEMOPEXIN-LIKE.
FT SITE 100 100 CYSTEINE SWITCH (BY SIMILARITY).
FT METAL 402 402 ZINC (CATALYTIC) (BY SIMILARITY).

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FT ACT_SITE 403 403 BY SIMILARITY.
FT METAL 406 406 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 412 412 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 519 707 BY SIMILARITY.
FT CONFLICT 2 2 S -> N (IN REF. 2).
FT CONFLICT 112 112 D -> E (IN REF. 2).
FT CONFLICT 326 327 AD -> LY (IN REF. 2).
FT CONFLICT 364 364 S -> G (IN REF. 2).
FT CONFLICT 441 441 H -> Q (IN REF. 2).
FT CONFLICT 472 472 S -> P (IN REF. 2).
FT CONFLICT 515 515 D -> V (IN REF. 2).
FT CONFLICT 551 551 N -> S (IN REF. 2).
FT CONFLICT 566 566 F -> L (IN REF. 2).
FT CONFLICT 568 568 S -> A (IN REF. 2).
FT CONFLICT 579 579 P -> S (IN REF. 2).
FT CONFLICT 589 589 LMAQ -> SGKK (IN REF. 2).
FT CONFLICT 597 597 S -> T (IN REF. 2).
FT CONFLICT 669 669 Q -> H (IN REF. 2).
SQ SEQUENCE 708 AA; 78610 MM; D51DCOD1B93A778C CRC64;

Query March 19.1%; Score 382; DB 1; Length 708;
Best Local Similarity 38.1%; Pred. No. 3.5e-24;
Matches 82; Conservative 25; Mismatches 80; Indels 28; Gaps 7;

QY 47 LGNGVSCQETAVTGTGGNSNGEPCVLPTFNGRTFVSCTEGRQDGLMCTTSNYEOD 106
Db 213 LGKG-----AVPEFTFGNANGACHPFTFEGRSYLSCTTIDGNDGKPMGCTTADYD 266
QY 107 QKISFCTDHTVLTGTGNSNGALCHPEFLYNNINNYDCTSEGRDNMKWCGTTONYAD 166
Db 267 RKVGFCESEN--LYTEHGNGDGKPCVFPFIEGHSYSACTKGRSDGYRCATTANYDQD 324
QY 167 QKSEPCMAAHELCITNE-GVM-----YRIGDQMDKHMDGHMRCCTCVNGGGEWTCT 220
Db 325 KADGFCPRADVTYTGNSAEMCVFPFVFGKYQS-----TCTSEGRSDGRMCA 375
QY 221 AYSQI--RDQCIYDITVYNTDFHKKHREGHML 252
Db 376 TTSNFDADKKWGFCEPDGYSI--FLVVAHFEHGL 408

RESULT 13
MM09 MOUSE STANDARD; PRT; 730 AA.
ID MM09 MOUSE STANDARD; PRT; 730 AA.
AC P41245: O06788: O9DC02:
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
CN MMP9 OR CLG4B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RA MEDLINE=941179406; PubMed=8132709;
RA Reponen P., Sahberg C., Munaut C., Thesleff I., Trygvaason K.;
RT "High expression of 92-kD type IV collagenase (gelatinase B) in the
RT osteoclast lineage during mouse development.";
RL J. Cell Biol. 124:1091-1102(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=93176173; PubMed=8382489;
RA Tanaka H., Hojo K., Yoshida H., Yoshioka T., Sugita K.;
RT "Molecular cloning and expression of the mouse 105-kDa gelatinase
RT cDNA.";
RL Biochem. Biophys. Res. Commun. 190:732-740(1993).

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RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=94062823; PubMed=8243459;
RA Masure S., Nys G., Fiten P., van Damme J., Odenakker G.;
RT "Mouse gelatinase B. cDNA cloning, regulation of expression and
RT glycosylation in WEHI-3 macrophages and gene organisation.";
RL Eur. J. Biochem. 218:129-141(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=94033534; PubMed=8219207;
RX Grabert T., Johnston J., Berliner N.;
RT "Cloning and expression of the cDNA encoding mouse neutrophil
RT gelatinase: demonstration of coordinate secondary granule protein
RT gene expression during terminal neutrophil maturation.";
RL Blood 82:3192-3197(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Irawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staudli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guzman S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetski S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP FUNCTION: COULD PLAY A ROLE IN BONE OSTEOCLASTIC RESORPTION.
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
CC types IV and V.
CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -1- SIMILARITY: THE CENTRAL DOMAIN SHOWS SIMILARITY TO THE TYPE-II
CC MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN
CC BINDS GELATIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
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CC or send an email to license@sib-swiss.ch).
CC -----
DR EMBL; Z27231; CA81745.1; -
DR EMBL; D12712; BAA0208.1; -
DR EMBL; X72794; CA51314.1; -
DR EMBL; X72795; CA51315.1; -
DR EMBL; S67830; AAB28942.1; -
DR EMBL; AK004651; BA823442.1; -
DR PIR; JCI456; JCI456.
DR HSSP; P08254; IUSN.
DR MEROPS; M10.004; -.
DR MGD; MGI:97011; Mmp9.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Matrixin.
DR InterPro; IPR006026; Nzn_MTpeptidse.

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DR InterPro; IPR006970; PT.
 DR InterPro; IPR006025; Zn_MTPeptidase.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; peptidase_M10; 1.
 DR Pfam; PF03933; peptidase_M10_N; 1.
 DR Pfam; PF04886; PT; 2.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRILIN.
 DR PRODOM; PD000995; FN_Type_II; 3.
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 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMC; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
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 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 KM Collagen degradation; Extracellular matrix; Repeat; Signal;
 KM Polymorphism.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT PROPEP 20 107 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 108 730 92 kDa TYPE IV COLLAGENASE.
 FT DOMAIN 223 280 FIBRONECTIN TYPE-II 1.
 FT DOMAIN 281 339 FIBRONECTIN TYPE-II 2.
 FT DOMAIN 340 397 FIBRONECTIN TYPE-II 3.
 FT DOMAIN 531 730 HEMOPEXIN-LIKE.
 FT SITE 100 100 CYSTEINE SWITCH (BY SIMILARITY).
 FT METAL 401 401 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT SITE 402 402 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 405 405 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 411 411 ZINC (CATALYTIC) (BY SIMILARITY).
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 534 729 BY SIMILARITY.
 FT VARIANT 514 514 A -> P.
 FT VARIANT 639 639 P -> L.
 FT VARIANT 711 711 P -> H.
 FT CONFLICT 20 20 A -> C (IN REF. 4).
 FT CONFLICT 25 26 P -> T (IN REF. 5).
 FT CONFLICT 466 466 P -> T (IN REF. 5).
 FT CONFLICT 514 514 A -> P (IN REF. 5).
 FT CONFLICT 639 639 P -> L (IN REF. 5).
 FT CONFLICT 711 711 P -> H (IN REF. 5).
 SQ SEQUENCE 730 AA; 80453 MW; E1911F6D5CCAC059 CRC64;

Query Match 19.1%; Score 382; DB 1; Length 730;
 Best local similarity 40.1%; Pred. No. 3.6e-24;
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QY 16 YGHCVTDSGVVSVGQWMLKT-----QGNKMTCTCLGNGVSCQETAVTGTGNSNGEP 70
 DB 241 YSACTTGG--RNDGTGWCSTTADYDQKFGFCP-----SERLYTE--HGNGGKRP 287

QY 71 CVLPFTNGRTPTSCCTEGRODGLWGSTSNTEODKYSFC--THTYLVNQTGNSN 127
 DB 288 CVPEPFIEGHSYSACTTKGRSDGRCWATYANDDLVYFCPTRYDATV--GNSA 343

QY 128 GALCHPEFLNNNNYDTCTSEGRDNMKWCGTTONYADOKFGFCP-----MAAHE- 178
 DB 344 GELCVFFVFLGKQYSCTSDGRDRGLMKCATTSNFTDKKMGFCPDQGYSLFLVAHEF 403

QY 179 -----EICTTNEGWMY 189
 DB 404 GHALGLDHSVPEALMY 420

RESULT 14
 MM09_BOVIN STANDARD; PRT; 712 AA.
 AC P52176;
 DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B
 DE (GELB).
 GN MMP9.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=95287902; PubMed=7770085;
 RA Baylis H.A., Hegson A., Hall R.;
 RT "infection with Theileria annulata induces expression of matrix
 RT metalloproteinase 9 and transcription factor AP-1 in bovine
 RT leucocytes.";
 RL Mol. Biochem. Parasitol. 69:211-222(1995).
 CC -1- FUNCTION: COULD PLAY A ROLE IN BONE OSTEOCLASTIC RESORPTION.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (by similarity).
 CC -1- SIMILARITY: THE CENTRAL DOMAIN SHOWS SIMILARITY TO THE TYPE-II
 CC MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN
 CC BINDS GELATIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
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 CC EMBL; X78324; CAAS5127.1; -.
 CC PIR; I46031; I46031.
 CC HSP; P22894; IJAP.
 CC MEROPS: M10.004; -.
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 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Matrilin.
 DR InterPro; IPR006026; Nzn_MTPeptidase.
 DR InterPro; IPR006970; PT.
 DR InterPro; IPR006025; Zn_MTPeptidase.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; hemopexin; 4.
 DR Pfam; PF00413; peptidase_M10; 1.
 DR Pfam; PF03933; peptidase_M10_N; 1.
 DR Pfam; PF04886; PT; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRILIN.
 DR PRODOM; PD000995; FN_Type_II; 3.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMC; 1.
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 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR Hydrolase; Metalloprotease; Glycoprotein; Zinc; Zymogen; Calcium;
 KM Collagen degradation; Extracellular matrix; Repeat; Signal;
 FT SIGNAL 1 19 BY SIMILARITY.
 FT PROPEP 20 106 ACTIVATION PEPTIDE.
 FT CHAIN 107 712 92 kDa TYPE IV COLLAGENASE.
 FT DOMAIN 223 280 FIBRONECTIN TYPE-II 1.
 FT DOMAIN 281 339 FIBRONECTIN TYPE-II 2.
 FT DOMAIN 340 397 FIBRONECTIN TYPE-II 3.
 FT DOMAIN 518 712 HEMOPEXIN-LIKE.

FT SITE 99 99 CYSTEINE SWITCH (BY SIMILARITY).
 FT METAL 401 401 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 402 402 BY SIMILARITY.
 FT METAL 405 405 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 411 411 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 521 709 BY SIMILARITY.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 Query Match 19.0%; Score 381; DB 1; Length 712;
 Best Local Similarity 40.8%; Pred. No. 4.2e-24;
 Matches 80; Conservative 25; Mismatches 53; Indels 38; Gaps 8;
 QY 16 YGHCVTDSGVVSYSGMOMLKT-----OGNKMQLCTCLNGVSCOEATVATOTYGGNSGEPC 71
 Db 241 YSACTTGG---RSDMLMCSFTADYDADRQ-----GCPSERLTYQ---DGNADGRPC 288
 QY 72 VLPTTNGRTYSCCTBERGROGHLMCSTTSYEDQKSF--TDHTVLVQTRGNSNG 128
 Db 289 VFPTFGQRTYSACTSDGRSDGRWCATTANYDDKLVGFCPTVDATV---TGNVAG 344
 QY 129 ALCHPEFLYNNHNTDCTSEGRDNMKCGTTONYVDADOKRGP--MAAE-- 178
 Db 345 ELGVFPFLCKEYSACTRBRNDGHLWCATTNFDKDKMGKPCPDQYSLFLVAHFEFG 404
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 Db 405 HALGLDHTSVPEALMY 420
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 ID MM09_HUMAN STANDARD; PRT; 707 AA.
 AC P14780; O9H421;
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB).
 GN MMP9 OR CLG4B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 20-37.
 RX MEDLINE=90008879; PubMed=2551898;
 RA Wilhelm S.M., Collier I.E., Warner B.L., Eisen A.Z., Grant G.A.,
 RA Goldberg G.I.;
 RA "SV40-transformed human lung fibroblasts secrete a 92-kDa type IV
 RT collagenase which is identical to that secreted by normal human
 RT macrophages.";
 RL J. Biol. Chem. 264:17213-17221(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91358433; PubMed=1653238;
 RA Huhtala P., Tuuttila A., Chow L.T., Lohi J., Keski-Oja J.,
 RA Tryggyrason K.;
 RA "Complete structure of the human gene for 92-kDa type IV collagenase.
 RT Divergent regulation of expression for the 92- and 72-kilodalton
 RT enzyme genes in HT-1080 cells.";
 RL J. Biol. Chem. 266:16485-16490(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91638749; PubMed=11780052;
 RA Jones M., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagdley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Buttill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cobby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dham P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leivaeslahti M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McHay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Treven A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RA "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISUB-B-cell;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra W.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-11 FROM N.A.
 RX MEDLINE=93149601; PubMed=8426746;
 RA Sato H., Seki M.;
 RA "Regulatory mechanism of 92 kDa type IV collagenase gene expression
 RT which is associated with invasiveness of tumor cells.";
 RL Oncogene 8:395-405(1993).
 RN [6]
 RP SEQUENCE OF 20-37.
 RX MEDLINE=91355647; PubMed=1653055;
 RA van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,
 RA Auwerx J., Van Damme J., Opdenacker G.;
 RA "The cytokine-protease connection: identification of a 96-kD TGF-
 RT gelatinase and regulation by interleukin-1 and cytokine inducers.";
 RL Cytokine 3:231-239(1991).
 RN [7]
 RP SEQUENCE OF 28-60.
 RC TISSUE=Neutrophils;
 RX MEDLINE=91249834; PubMed=1645657;
 RA Masure S., Proost P., van Damme J., Opdenacker G.;
 RA "Purification and identification of 91-kDa neutrophil gelatinase.
 RT Release by the activating peptide interleukin-8.";
 RL Eur. J. Biochem. 198:391-398(1991).
 RN [8]
 RP CHARACTERIZATION.
 RA Kang K., Lee D.-H.;
 RA "Purification and characterization of human 92-kDa type IV collagenase

RT (gelatinase B).";
 RL Exp. Mol. Med. 28:161-165(1996).
 RN [9]
 RP 3D-STRUCTURE MODELING.
 RA Mallena S.C., Sagatkar R.D.;
 RT "Theoretical model of human type IV collagenase precursor.";
 RL Submitted (APR-2002) to the PDB data bank.
 RN [10]
 RP VARIANTS VAL-20; LYS-82 AND GLN-279.
 RX MEDLINE=20065865; Pubmed=10598806;
 RA Zhang B., Henney A., Eriksson P., Hamsten A., Watkins H., Ye S.;
 RT "Genetic variation at the matrix metalloproteinase-9 locus on
 chromosome 20q12.2-13.1.";
 RL Hum. Genet. 105:418-423(1999).
 CC -1- FUNCTION: COULD PLAY A ROLE IN BONE OSTEOCLASTIC RESORPTION.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (by similarity).
 CC -1- SUBUNIT: EXISTS AS MONOMER, DISULFIDE-LINKED HOMODIMER, AND AS A
 CC HETERODIMER WITH A 25 KDA PROTEIN. MACROPHAGES AND TRANSFORMED
 CC CELL LINES PRODUCE ONLY THE MONOMERIC FORM.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY NORMAL ALVEOLAR MACROPHAGES AND
 CC GRANULOCYTES.
 CC -1- SIMILARITY: THE CENTRAL DOMAIN SHOWS SIMILARITY TO THE TYPE-II
 CC MOTIF OF COLLAGEN-BINDING DOMAIN OF FIBRONECTIN. THIS DOMAIN
 CC BINDS GELATIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -----
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 CC -----
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 DR EMBL: D10051; BA20967.1; -;
 DR EMBL: AL162458; CAC10459.1; -;
 DR EMBL: BC006093; AAH06093.1; -;
 DR PIR: A34458; A34458.
 DR PDB: 1LKG; 15-MAY-02.
 DR PDB: 1GKC; 16-MAY-02.
 DR PDB: 1GKD; 16-MAY-02.
 DR PDB: 1ITV; 04-SEP-02.
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 DR InterPro: IPR001818; Matrixin.
 DR InterPro: IPR006026; Nzn_MTPeptide.
 DR InterPro: IPR006970; PT.
 DR InterPro: IPR006025; Zn_MTPeptide.
 DR Pfam: PF00040; fn2_3.
 DR Pfam: PF00045; hemopexin; 4.
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 DR PRINTS: PR00138; MATRIXIN.
 DR ProDom: PD000995; FN_Type_II; 3.
 DR SMART: SM00059; FN2_3.
 DR SMART: SM00120; HX; 4.
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 DR PROSITE: PS00023; FIBRONECTIN_2; 3.

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 DR PROSITE: PS00546; CYSTEINE SWITCH; 1.
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 KW Polymorphism; 3D-structure.
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 FT DOMAIN 223 280
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 DB 241 YSACTTDG---RSDGLPWCSTTANVD---TDPRFGCPSERLYTR--DGNADSKPCQFPF 292
 QY 76 TYNGRTFYSCTTEGRDGHLMCSTTSNYEQDKYSPC---TDHTVLVQTRGNSNGALCH 132
 DB 293 IFGGQGSYSACTTDGRSDGRWCATTANYDRDKLFGCPTRADSTW-----GGSAGELCV 348
 QY 133 FPFLLNNHNYTDCTSGRDNKMKCGTTONYDADQKFGCP-----MAAHE----- 178
 DB 349 FPFPLFGKEYSCTSGRGRGLMCATTSNFDSDKWKMGCPDQGYSLFVVAHEFGHALG 408
 QY 179 -EICTNEGVMY 189
 DB 409 LDHSSVPEALMY 420

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 Job time : 18 secs

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PI Ishikawa T, Kicajima T;
XX WPI; 2000-565375/52.
XX N-PSDB; AAA64263.
XX
PT Collagen-binding active polypeptide for use in an agent for enabling
PT topical retention or sustained release of a physiologically active
PT peptide or physiological activity-imparting agent comprises a
XX fibronectin peptide -
XX
PS Disclosure; Page 113-115; 135pp; English.
XX
CC The present sequence represents a modified fibronectin collagen-
CC binding domain. The protein is used to construct a collagen-binding
CC physiologically active polypeptide. This polypeptide comprises a
CC peptide from fibronectin ligated to a physiologically active peptide.
CC The polypeptides are used in an agent for enabling topical retention or
CC sustained release of a physiologically active peptide or physiological
CC activity-imparting agent. They may be used in gene therapy and in
CC tissue regeneration.
XX
SQ Sequence 343 AA;
XX
Query Match 100.0%; Score 2002; DB 21; Length 343;
Best Local Similarity 100.0%; Pred. No. 3e-143;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVYQPPHPPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
Db 1 MAAVYQPPHPPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPTFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDQKYSFCTDHTVLVQ 120
Db 61 TYGNSNGEPCVLPTFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTQNYADQKFGCPMAAHEI 180
Db 121 TRGNSNGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTQNYADQKFGCPMAAHEI 180
QY 181 CTTEGWWYRIGDQMDKQHDGMHMRCTCVNGNGRGEMTCLAYSQLRDQCIYDDITVNVND 240
Db 181 CTTEGWWYRIGDQMDKQHDGMHMRCTCVNGNGRGEMTCLAYSQLRDQCIYDDITVNVND 240
QY 241 TFHRRHEGHMLNCTCFGQGRGKWCDPVDCQDSEGTFTFYQIDSMERYVHGVYQCYC 300
Db 241 TFHRRHEGHMLNCTCFGQGRGKWCDPVDCQDSEGTFTFYQIDSMERYVHGVYQCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVVEFTTETPSQNSHPIDWLE 343
Db 301 YGRGIGEMHCOPLOTYPSSSGPVVEFTTETPSQNSHPIDWLE 343
RESULT 2
AAB07961
ID AAB07961 standard; Protein; 343 AA.
XX
AC AAB07961;
XX
DT 12-AUG-2002 (first entry)
XX
DE Modified human fibronectin collagen-binding domain.
XX
KW Osteogenesis; drug delivery system; DDS; collagen; osteopathic; human;
XX fibronectin.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN JP2002058485-A.
XX
PD 26-FEB-2002.
XX
FT 16-AUG-2000; 2000JP-0246744.

XX
PR 16-AUG-2000; 2000JP-0246744.
XX
PA (TERU) TERUMO CORP.
XX
DR WPI; 2002-438612/47.
XX N-PSDB; ABL41020.
XX
PT Novel osteogenesis stimulating fused protein having collagen avidity
PT used as an osteogenesis stimulator and a localizing agent -
XX
PS Disclosure; Page 17-18; 30pp; Japanese.
XX
CC The invention provides an osteogenesis stimulating fused protein (I) for
CC a drug delivery system (DDS) of osteogenic factor, having collagen
CC avidity and polypeptides homologous to collagen avidity domain or its
CC modified peptides. (I) is used for stimulation of osteogenesis, a
CC localizing agent and a slow releasing agent for a drug delivery system.
CC The present sequence represents a modified human fibronectin collagen-
CC binding domain.
XX
SQ Sequence 343 AA;
XX
Query Match 100.0%; Score 2002; DB 23; Length 343;
Best Local Similarity 100.0%; Pred. No. 3e-143;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVYQPPHPPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
Db 1 MAAVYQPPHPPPPYGHCVTDSGVVSVGMQMLKTQGNKQMLCTCLGNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPTFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDQKYSFCTDHTVLVQ 120
Db 61 TYGNSNGEPCVLPTFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDQKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTQNYADQKFGCPMAAHEI 180
Db 121 TRGNSNGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTQNYADQKFGCPMAAHEI 180
QY 181 CTTEGWWYRIGDQMDKQHDGMHMRCTCVNGNGRGEMTCLAYSQLRDQCIYDDITVNVND 240
Db 181 CTTEGWWYRIGDQMDKQHDGMHMRCTCVNGNGRGEMTCLAYSQLRDQCIYDDITVNVND 240
QY 241 TFHRRHEGHMLNCTCFGQGRGKWCDPVDCQDSEGTFTFYQIDSMERYVHGVYQCYC 300
Db 241 TFHRRHEGHMLNCTCFGQGRGKWCDPVDCQDSEGTFTFYQIDSMERYVHGVYQCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVVEFTTETPSQNSHPIDWLE 343
Db 301 YGRGIGEMHCOPLOTYPSSSGPVVEFTTETPSQNSHPIDWLE 343
RESULT 3
AAB08509
ID AAB08509 standard; Protein; 400 AA.
XX
AC AAB08509;
XX
DT 20-DEC-2000 (first entry)
XX
DE Hybrid of fibronectin collagen-binding domain/epidermal growth factor.
XX
KW Fibronectin; collagen-binding domain; sustained release; gene therapy;
XX physiologically active polypeptide; topical retention; chimera;
XX tissue regeneration; epidermal growth factor.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 2..341
FT Misc-difference 343..347
FT "human fibronectin collagen-binding domain"

FT /note= "enterokinase recognition sequence"
FT Protein 348.400
XX /note= "epidermal growth factor"
XX
XX WO200049159-A1.
XX
XX 24-AUG-2000.
XX
XX 21-FEB-2000; 2000WO-JP00964.
XX
XX 19-FEB-1999; 99JP-0041913.
XX PR 01-NOV-1999; 99JP-0311364.
XX
XX (TERU) TERUMO CORP.
XX
XX Ishikawa T, Kiteajima T;
XX WPI; 2000-565375/52.
XX DR N-PSDB; AAA64271.
XX
XX Collagen-binding active polypeptide for use in an agent for enabling
PT topical retention or sustained release of a physiologically active
PT peptide or physiological activity-impacting agent comprises a
PT fibronectin peptide -
XX
XX Disclosure; Page 122-124; 135pp; English.
XX
XX The present sequence represents a hybrid polypeptide, comprising a
CC modified human fibronectin collagen-binding domain and a modified
CC human epidermal growth factor with an enterokinase recognition
CC sequence. The protein is representative of collagen-binding
CC physiologically active polypeptides of the invention. These
CC polypeptides comprise a peptide from fibronectin ligated to a
CC physiologically active peptide. The polypeptides are used in an
CC agent for enabling topical retention or sustained release of a
CC physiologically active peptide or physiological activity-impacting
CC agent. They may be used in gene therapy and in tissue regeneration.
XX
XX Sequence 400 AA;
SQ
Query Match 99.3%; Score 1999; DB 21; Length 400;
Best Local Similarity 99.7%; Pred. No. 6e-143;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAYVQPPHPPPPHGHCTDSDGVYVSGMQLTKQGNKMLCTCLGNVSCQETAVTQ 60
DB 1 MAAYVQPPHPPPPHGHCTDSDGVYVSGMQLTKQGNKMLCTCLGNVSCQETAVTQ 60
QY TYGNSNGEBCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEODKYSFCTDHTVLVQ 120
DB TYGNSNGEBCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEODKYSFCTDHTVLVQ 120
QY 61 TYGNSNGEBCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEODKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEBCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEODKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADQKFCFPMAAHEE1 180
DB 121 TRGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADQKFCFPMAAHEE1 180
QY 121 TRGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADQKFCFPMAAHEE1 180
DB 121 TRGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADQKFCFPMAAHEE1 180
QY 181 CTNEGMYRIGDMQKDHMMHMRCTCVGNRGEWTCIAYSQLRQCCIVDDITVNVND 240
DB 181 CTNEGMYRIGDMQKDHMMHMRCTCVGNRGEWTCIAYSQLRQCCIVDDITVNVND 240
QY 181 CTNEGMYRIGDMQKDHMMHMRCTCVGNRGEWTCIAYSQLRQCCIVDDITVNVND 240
DB 181 CTNEGMYRIGDMQKDHMMHMRCTCVGNRGEWTCIAYSQLRQCCIVDDITVNVND 240
QY 241 TFHKRHEBGLMNLCTCFGQGRGKMKCDPVQCCDSEGTGYQIGDSSEKTVHGVRYCCYC 300
DB 241 TFHKRHEBGLMNLCTCFGQGRGKMKCDPVQCCDSEGTGYQIGDSSEKTVHGVRYCCYC 300
QY 301 YGRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQMLE 343
DB 301 YGRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQMLE 343
RESULT 4
ABB07964 standard; Protein; 461 AA.
XX

AC ABB07964;
XX
XX 12-AUG-2002 (first entry)
XX
XX Human fibronectin collagen-binding domain/BMP2 hybrid protein.
XX DE
XX Osteogenesis; drug delivery system; DSS; collagen; osteopathic; human;
XX KM fibronectin; BMP2; hybrid; fusion protein.
XX
XX Homo sapiens.
XX OS Synthetic.
XX JP2002058485-A.
XX
XX 26-FEB-2002.
XX
XX 16-AUG-2000; 2000JP-0246744.
XX
XX 16-AUG-2000; 2000JP-0246744.
XX PR 16-AUG-2000; 2000JP-0246744.
XX
XX (TERU) TERUMO CORP.
XX
XX WPI; 2002-438612/47.
XX DR N-PSDB; ABL41027.
XX
XX Novel osteogenesis stimulating fused protein having collagen avidity
PT used as an osteogenesis stimulator and a localizing agent -
XX
XX Disclosure; Page 23-25; 30pp; Japanese.
XX
XX The invention provides an osteogenesis stimulating fused protein (I) for
CC a drug delivery system (DSS) of osteogenic factor, having collagen
CC avidity and polypeptides homologous to collagen avidity domain or its
CC modified peptides. (I) is used for stimulation of osteogenesis, a
CC localizing agent and a slow releasing agent for a drug delivery system.
CC The present sequence represents a human fibronectin collagen-binding
CC domain/human BMP2 hybrid protein.
XX
XX Sequence 461 AA;
SQ
Query Match 99.3%; Score 1999; DB 23; Length 461;
Best Local Similarity 99.7%; Pred. No. 7e-143;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAYVQPPHPPPPHGHCTDSDGVYVSGMQLTKQGNKMLCTCLGNVSCQETAVTQ 60
DB 1 MAAYVQPPHPPPPHGHCTDSDGVYVSGMQLTKQGNKMLCTCLGNVSCQETAVTQ 60
QY TYGNSNGEBCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEODKYSFCTDHTVLVQ 120
DB TYGNSNGEBCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEODKYSFCTDHTVLVQ 120
QY 61 TYGNSNGEBCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEODKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEBCVLPFTYNGRTFYSCTTEGRDGHLMCTTSNTEODKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADQKFCFPMAAHEE1 180
DB 121 TRGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADQKFCFPMAAHEE1 180
QY 121 TRGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADQKFCFPMAAHEE1 180
DB 121 TRGNSNGALCHFPFLYNNHNYTDCTSEGRDMMKMGCTTQNDADQKFCFPMAAHEE1 180
QY 181 CTNEGMYRIGDMQKDHMMHMRCTCVGNRGEWTCIAYSQLRQCCIVDDITVNVND 240
DB 181 CTNEGMYRIGDMQKDHMMHMRCTCVGNRGEWTCIAYSQLRQCCIVDDITVNVND 240
QY 181 CTNEGMYRIGDMQKDHMMHMRCTCVGNRGEWTCIAYSQLRQCCIVDDITVNVND 240
DB 181 CTNEGMYRIGDMQKDHMMHMRCTCVGNRGEWTCIAYSQLRQCCIVDDITVNVND 240
QY 241 TFHKRHEBGLMNLCTCFGQGRGKMKCDPVQCCDSEGTGYQIGDSSEKTVHGVRYCCYC 300
DB 241 TFHKRHEBGLMNLCTCFGQGRGKMKCDPVQCCDSEGTGYQIGDSSEKTVHGVRYCCYC 300
QY 301 YGRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQMLE 343
DB 301 YGRGIGEMHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQMLE 343
RESULT 5
ABB07965 standard; Protein; 473 AA.
XX

AC AAB07965;
XX
DT 12-AUG-2002 (first entry)
XX
DE Human fibronectin collagen-binding domain/BMP7 hybrid protein.
XX
KW Osteogenesis; drug delivery system; DDS; collagen; osteopathic; human;
XX fibronectin; BMP7; hybrid; fusion protein.
XX Homo sapiens.
OS Synthetic.
XX JP2002058485-A.
XX
XX 26-FEB-2002.
XX
XX 16-AUG-2000; 2000JP-0246744.
XX
XX 16-AUG-2000; 2000JP-0246744.
XX
XX (TERU) TERUMO CORP.
XX
XX WPI: 2002-438612/47.
XX N-PSDB: ABL41028.
XX
XX Novel osteogenesis stimulating fused protein having collagen avidity
XX used as an osteogenesis stimulator and a localizing agent -
XX
XX Disclosure; Page 26-28; 30pp; Japanese.
XX
XX The invention provides an osteogenesis stimulating fused protein (1) for
XX a drug delivery system (DDS) of osteogenic factor, having collagen
XX avidity and polypeptides homologous to collagen avidity domain or its
XX modified peptide. (1) is used for stimulation of osteogenesis, a
XX localizing agent and a slow releasing agent for a drug delivery system.
XX The present sequence represents a human fibronectin collagen-binding
XX domain/human BMP7 hybrid protein.
XX
XX Sequence 473 AA;
SQ
Query Match 99.9%; Score 1999; DB 23; Length 473;
Best Local Similarity 99.7%; Pred. No. 7.2e-143; Indels 0; Gaps 0;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVYQPPHPPYGHCVTDGSGVYVSVGMQMLKTGKNKMLCTCLGNGVSCQETAVTQ 60
DB 1 MAAVYQPPHPPYGHCVTDGSGVYVSVGMQMLKTGKNKMLCTCLGNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHPFLVNNHNYTDTSGRRDNMKMGCTTONYADOKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHPFLVNNHNYTDTSGRRDNMKMGCTTONYADOKFGFCPMAAHEI 180
QY 181 CTTEGVYRIGDQMDKQDMGMMARCTCVGNGRGEMTCLIAVSQLRDQCIYDDITVYVND 240
DB 181 CTTEGVYRIGDQMDKQDMGMMARCTCVGNGRGEMTCLIAVSQLRDQCIYDDITVYVND 240
QY 241 TFHRRHEGHLNCTCFGQGRGKWCDDVQCCODSETGYQIGDSWEKYYHGVAYCYC 300
DB 241 TFHRRHEGHLNCTCFGQGRGKWCDDVQCCODSETGYQIGDSWEKYYHGVAYCYC 300
QY 301 YGRGIGEHCOPLQTYPSSSGPVEVFTETPSQPSHPIOMLE 343
DB 301 YGRGIGEHCOPLQTYPSSSGPVEVFTETPSQPSHPIOMLE 343
301 YGRGIGEHCOPLQTYPSSSGPVEVFTETPSQPSHPIOMLE 343
301 YGRGIGEHCOPLQTYPSSSGPVEVFTETPSQPSHPIOMLE 343
RESULT 6
AAB08508
ID. AAB08508 standard; Protein; 501 AA.
XX

AC AAB08508;
XX
DT 20-DEC-2000 (first entry)
XX
DE Hybrid of fibronectin collagen-binding domain/fibroblast growth factor.
XX
KW Fibronectin; collagen-binding domain; sustained release; gene therapy;
XX physiologically active polypeptide; topical retention; chimera;
XX tissue regeneration; fibroblast growth factor.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Protein 2..341
XX FT /note= "human fibronectin collagen-binding domain"
XX FT Misc-difference 343..347
XX FT /note= "enterokinase recognition sequence"
XX FT Protein 348..501
XX FT /note= "fibroblast growth factor"
XX
XX WO200049159-A1.
XX
XX 24-AUG-2000.
XX
XX 21-FEB-2000; 2000WO-JP00964.
XX
XX 19-FEB-1999; 99JP-0041913.
XX 01-NOV-1999; 99JP-0311364.
XX
XX (TERU) TERUMO CORP.
XX
XX Ishikawa T, Kitajima T;
XX
XX WPI: 2000-565375/52.
XX N-PSDB: AAA64270.
XX
XX Collagen-binding active polypeptide for use in an agent for enabling
XX topical retention or sustained release of a physiologically active
XX peptide or physiological activity-imparting agent comprises a
XX fibronectin peptide -
XX
XX Disclosure; Page 118-121; 135pp; English.
XX
XX The present sequence represents a hybrid polypeptide, comprising a
XX modified human fibronectin collagen-binding domain and a modified
XX human fibroblast growth factor with an enterokinase recognition
XX sequence. The protein is representative of collagen-binding
XX physiologically active polypeptides of the invention. These
XX polypeptides comprise a peptide from fibronectin ligated to a
XX physiologically active peptide. The polypeptides are used in an
XX agent for enabling topical retention or sustained release of a
XX physiologically active peptide or physiological activity-imparting
XX agent. They may be used in gene therapy and in tissue regeneration.
XX
XX Sequence 501 AA;
SQ
Query Match 99.9%; Score 1999; DB 21; Length 501;
Best Local Similarity 99.7%; Pred. No. 7.7e-143; Indels 0; Gaps 0;
Matches 342; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAVYQPPHPPYGHCVTDGSGVYVSVGMQMLKTGKNKMLCTCLGNGVSCQETAVTQ 60
DB 1 MAAVYQPPHPPYGHCVTDGSGVYVSVGMQMLKTGKNKMLCTCLGNGVSCQETAVTQ 60
QY 61 TYGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTDHTVLVQ 120
DB 61 TYGNSNGEPCVLPFTYNGRTFYSCCTEGRODGHLMCSTTSNYEDOKYSFCTDHTVLVQ 120
QY 121 TRGNSNGALCHPFLVNNHNYTDTSGRRDNMKMGCTTONYADOKFGFCPMAAHEI 180
DB 121 TRGNSNGALCHPFLVNNHNYTDTSGRRDNMKMGCTTONYADOKFGFCPMAAHEI 180

QY 181 CTNNEGVMYRIGDQMDKQDMGHMMRCTCVNGRGEMTCLAYSQLRDQCIIVDDITYNVND 240
DB 181 CTNNEGVMYRIGDQMDKQDMGHMMRCTCVNGRGEMTCLAYSQLRDQCIIVDDITYNVND 240
QY 241 TFKRHEEGHMLNCTCGQGRGRWKCDPVQCCDSSETGFYQIGDSMEKYVHGVRQCYC 300
DB 241 TFKRHEEGHMLNCTCGQGRGRWKCDPVQCCDSSETGFYQIGDSMEKYVHGVRQCYC 300
QY 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPHOMLE 343
DB 301 YGRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPHOMLE 343
RESULT 7
ABG22275
ID ABG22275 standard; Protein; 1173 AA.
XX ABG22275;
AC
XX 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22266.
XX
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX MO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS86462.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 52634; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG0010-ABG0377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

SEQ Sequence 1173 AA;
Query Match 99.3%; Score 1988; DB 22; Length 1173;
Best Local Similarity 100.0%; Pred. No. 1,4e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAYVQPPHQPPEYGHCVTDSGVVYSVGMQLKTQGNKMLCTCLGNVSCQETAVTQT 61
DB 245 AAYVQPPHQPPEYGHCVTDSGVVYSVGMQLKTQGNKMLCTCLGNVSCQETAVTQT 304
QY 62 YGNSNGEPCVLPFTYNGRTFFYCTTGRDGHLMCSTTNYEDQKYSFCTDHTVAVQT 121
DB 305 YGNSNGEPCVLPFTYNGRTFFYCTTGRDGHLMCSTTNYEDQKYSFCTDHTVAVQT 364
QY 122 RGNNSGALCHPEPLVNNHNYTDCSTSGRDNMKCGTTONYADQKFGCPMAAHEIC 181
DB 365 RGNNSGALCHPEPLVNNHNYTDCSTSGRDNMKCGTTONYADQKFGCPMAAHEIC 424
QY 182 TTNEGVMYRIGDQMDKQDMGHMMRCTCVNGRGEMTCLAYSQLRDQCIIVDDITYNVNDT 241
DB 425 TTNEGVMYRIGDQMDKQDMGHMMRCTCVNGRGEMTCLAYSQLRDQCIIVDDITYNVNDT 484
QY 242 FHKRHEEGHMLNCTCGQGRGRWKCDPVQCCDSSETGFYQIGDSMEKYVHGVRQCYC 301
DB 485 FHKRHEEGHMLNCTCGQGRGRWKCDPVQCCDSSETGFYQIGDSMEKYVHGVRQCYC 544
QY 302 GRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPHOM 341
DB 545 GRGIGEMHCOPLOTYPSSSGPVEVFTTETPSQNSHPHOM 584
RESULT 8
AAM38647
ID AAM38647 standard; Protein; 2265 AA.
XX
AC AAM38647;
XX
DT 22-OCT-2001 (first entry)
XX
XX
DE Human polypeptide SEQ ID NO 1792.
XX
XX Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
OS Homo sapiens.
XX
XX MO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000MO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI57803.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX
PS Example 3; SEQ ID NO 1792; 10078bp; English.
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA157798-AA161369) with nootropic,
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 2265 AA;
Query Match 99.3%; Score 1988; DB 22; Length 2265;
Best Local Similarity 100.0%; Pred. No. 2.9e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAVYQPHPPPPYGHGCVTDGSGVYVSVGMOMLKTQGNKQMLCTCLGNGVSCQETAVYTQT 61
DB 291 AAVYQPHPPPPYGHGCVTDGSGVYVSVGMOMLKTQGNKQMLCTCLGNGVSCQETAVYTQT 350
QY 62 YGNSNGPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNVEDOKXSFCTDHTVLVQT 121
DB 351 YGNSNGPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNVEDOKXSFCTDHTVLVQT 410
QY 122 RGSNSGALCHFPFLYNNHNYTDCSTSEGRDNMKCGTTONYADADOKRFGCPMAHEBIC 181
DB 411 RGSNSGALCHFPFLYNNHNYTDCSTSEGRDNMKCGTTONYADADOKRFGCPMAHEBIC 470
QY 182 TTNGVWYRIGDQMDKDHMGHMRCTCVNGRGSEWTCIAYSQLRDQCIYVDITVYNDT 241
DB 471 TTNGVWYRIGDQMDKDHMGHMRCTCVNGRGSEWTCIAYSQLRDQCIYVDITVYNDT 530
QY 242 FHKHSEGHMNCCTFCGGRGRMKCDPVDOCDSETGFYQIGSWEXYHGVRYQCYCY 301
DB 531 FHKHSEGHMNCCTFCGGRGRMKCDPVDOCDSETGFYQIGSWEXYHGVRYQCYCY 590
QY 302 GRGIGEWHCOPLOQTPSSSGPVEVFTTETPSQPNSHPIOW 341
DB 591 GRGIGEWHCOPLOQTPSSSGPVEVFTTETPSQPNSHPIOW 630
RESULT 9
ID AA157798 standard; Protein; 2330 AA.
AA157798
AC AA157798;
XX
XX 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 1791.
XX
XX Human, nootropic, immunosuppressant, cytoskeletal, gene therapy, cancer,
XX peripheral nervous system, neuropathy, central nervous system, CNS;
XX Alzheimer's, Parkinson's disease, Huntington's disease, haemostatic,
XX amyotrophic lateral sclerosis, Shy-Drager Syndrome, chemotactic,
XX chemokinetic, thrombolytic, drug screening, arthritis, inflammation,
XX leukaemia.
XX Homo sapiens.
XX

FN WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HSE-) HSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AD, Yang Y, Zhang J;
XX Zhao QH, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX N-PSDB; AA157802.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Example 3; SEQ ID NO 1791; 10078bp; English.
PS
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA157798-AA161369) with nootropic,
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 2330 AA;
Query Match 99.3%; Score 1988; DB 22; Length 2330;
Best Local Similarity 100.0%; Pred. No. 3e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAVYQPHPPPPYGHGCVTDGSGVYVSVGMOMLKTQGNKQMLCTCLGNGVSCQETAVYTQT 61
DB 291 AAVYQPHPPPPYGHGCVTDGSGVYVSVGMOMLKTQGNKQMLCTCLGNGVSCQETAVYTQT 350
QY 62 YGNSNGPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNVEDOKXSFCTDHTVLVQT 121
DB 351 YGNSNGPCVLPFTYNGRTFYSCTTEGRDGHLMCSTTSNVEDOKXSFCTDHTVLVQT 410
QY 122 RGSNSGALCHFPFLYNNHNYTDCSTSEGRDNMKCGTTONYADADOKRFGCPMAHEBIC 181
DB 411 RGSNSGALCHFPFLYNNHNYTDCSTSEGRDNMKCGTTONYADADOKRFGCPMAHEBIC 470
QY 182 TTNGVWYRIGDQMDKDHMGHMRCTCVNGRGSEWTCIAYSQLRDQCIYVDITVYNDT 241
DB 471 TTNGVWYRIGDQMDKDHMGHMRCTCVNGRGSEWTCIAYSQLRDQCIYVDITVYNDT 530
QY 242 FHKHSEGHMNCCTFCGGRGRMKCDPVDOCDSETGFYQIGSWEXYHGVRYQCYCY 301
DB 531 FHKHSEGHMNCCTFCGGRGRMKCDPVDOCDSETGFYQIGSWEXYHGVRYQCYCY 590
QY 302 GRGIGEWHCOPLOQTPSSSGPVEVFTTETPSQPNSHPIOW 341

PS Example 3; SEQ ID NO 1793; 10078bp; English.
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nootropic.
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX
SQ Sequence 2386 AA;
Query Match 99.3%; Score 1988; DB 22; Length 2386;
Best Local Similarity 100.0%; Pred. No. 3,1e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAVYQOPHPQPPYGHCVTDGIVVYSGVMQMLTKQGNKMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQOPHPQPPYGHCVTDGIVVYSGVMQMLTKQGNKMLCTCLGNGVSCQETAVTQT 350
QY 62 YGGSNBEPCVLPPTYNGRFTYSCCTEGRODGHLMCSTTSNYEDOKXSFCTDHTVLVQT 121
DB 351 YGGSNBEPCVLPPTYNGRFTYSCCTEGRODGHLMCSTTSNYEDOKXSFCTDHTVLVQT 410
QY 122 RGSNSNGLCHFPPLNNHNTTDCSTSEGRDNMKCGTTQYVDADOKFGFPMANHEBIC 181
DB 411 RGSNSNGLCHFPPLNNHNTTDCSTSEGRDNMKCGTTQYVDADOKFGFPMANHEBIC 470
QY 182 TTNEGVMYRIGDQDKDHDMGMMRCTCVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 241
DB 471 TTNEGVMYRIGDQDKDHDMGMMRCTCVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 530
QY 242 FHKHEBEGHMLNCTCFQSGRGRMKCDPVDOCDSETGTFYQIGSWEXYVAGVAYQCYCY 301
DB 531 FHKHEBEGHMLNCTCFQSGRGRMKCDPVDOCDSETGTFYQIGSWEXYVAGVAYQCYCY 590
QY 302 GRGIGEMHCOPLQTYPSSSGPVEVFTTETPSQPNSHPIOW 341
DB 591 GRGIGEMHCOPLQTYPSSSGPVEVFTTETPSQPNSHPIOW 630
RESULT 12
AAB50377
ID AAB50377 standard; Protein; 2446 AA.
AC AAB50377;
XX
XX 12-MAR-2001 (first entry)
XX
XX Human fibronectin.
XX
XX Human; FN; fibronectin; prostate cancer; biallelic marker; diagnosis.
XX
XX Homo sapiens.
XX
XX W0200058509-A2.
XX
XX 05-OCT-2000.
XX
XX 28-MAR-2000; 2000WO-1B00431.
XX
XX 29-MAR-1999; 99US-0126780.
XX
XX (GEST) GENSET.
XX

XX
XX Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A;
XX
XX WPI: 2000-594647/56.
XX
XX N-PSDB; AAC89889.
XX
XX Fibronectin polynucleotide and polypeptide sequences, useful for
XX determining the predisposition of individuals to cancer, such as
XX prostate cancer -
XX
PS Claim 4; Page 185-190; 208pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
XX or purified recombinant polynucleotide comprising a contiguous span of at
XX least 12 nucleotides of a fibronectin (FN) gene. The methods and
XX sequences are useful for determining the predisposition of individuals to
XX cancer such as prostate cancer and for the prognosis/detection of an
XX eventual treatment response to therapeutic agents acting against prostate
XX cancer. Biallelic markers allow association studies to be performed
XX to identify genes involved in complex traits.
XX
XX
SQ Sequence 2446 AA;
Query Match 99.3%; Score 1988; DB 21; Length 2446;
Best Local Similarity 100.0%; Pred. No. 3,2e-141;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAVYQOPHPQPPYGHCVTDGIVVYSGVMQMLTKQGNKMLCTCLGNGVSCQETAVTQT 61
DB 291 AAVYQOPHPQPPYGHCVTDGIVVYSGVMQMLTKQGNKMLCTCLGNGVSCQETAVTQT 350
QY 62 YGGSNBEPCVLPPTYNGRFTYSCCTEGRODGHLMCSTTSNYEDOKXSFCTDHTVLVQT 121
DB 351 YGGSNBEPCVLPPTYNGRFTYSCCTEGRODGHLMCSTTSNYEDOKXSFCTDHTVLVQT 410
QY 122 RGSNSNGLCHFPPLNNHNTTDCSTSEGRDNMKCGTTQYVDADOKFGFPMANHEBIC 181
DB 411 RGSNSNGLCHFPPLNNHNTTDCSTSEGRDNMKCGTTQYVDADOKFGFPMANHEBIC 470
QY 182 TTNEGVMYRIGDQDKDHDMGMMRCTCVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 241
DB 471 TTNEGVMYRIGDQDKDHDMGMMRCTCVNGRGEMTCTIAVSQLRDQCTIVDDIYNNVDT 530
QY 242 FHKHEBEGHMLNCTCFQSGRGRMKCDPVDOCDSETGTFYQIGSWEXYVAGVAYQCYCY 301
DB 531 FHKHEBEGHMLNCTCFQSGRGRMKCDPVDOCDSETGTFYQIGSWEXYVAGVAYQCYCY 590
QY 302 GRGIGEMHCOPLQTYPSSSGPVEVFTTETPSQPNSHPIOW 341
DB 591 GRGIGEMHCOPLQTYPSSSGPVEVFTTETPSQPNSHPIOW 630
RESULT 13
AAO17353
ID AAO17353 standard; protein; 2386 AA.
AC AAO17353;
XX
XX 19-JUL-2002 (first entry)
XX
XX Human fibronectin.
XX
XX Human; endometriosis; DNA chip; fibronectin; p27; reticulocalbin;
XX aldehyde dehydrogenase 6; gravin; phospholipase C epsilon; elastin;
XX insulin-like growth factor binding protein-2; alpha-2 type IV collagen;
XX transmembrane receptor PTK7; collagen type XVIII alpha 1;
XX platelet derived growth factor receptor alpha; laminin M chain;
XX subtilisin like protein PACE4; nidogen.
XX
XX Homo sapiens.
XX
XX EP1191107-A2.
XX

PD 27-MAR-2002.
XX
XX 21-AUG-2001; 2001EP-0250300.
XX
XX 25-SEP-2000; 2000DE-1048633.
XX
XX (SCHD) SCHERING AG.
XX
XX Hess-stump H, Haendler B, Kraetzschmar J, Kreft B, Winterhager E,
PI Regidor P, Scotti S;
XX WPI; 2002-317413/36.
XX
XX In vitro diagnosis and monitoring of endometriosis, comprises
PT detecting reduced expression of specific gene products, e.g. from the
PT fibronectin gene -
XX
XX Claim 1; Page 9-10; 21pp; German.
XX
XX The present invention relates to a method for the in vitro diagnosis of
CC endometriosis by determining the amount of gene product from at least one
CC specific gene in a patient sample and comparing this with the amount of
CC gene product in a control sample. A reduced level is indicative of
CC endometriosis. The gene products may be fibronectin, p27, reticulocalbin,
CC aldehyde dehydrogenase 6, gravin, phospholipase C epsilon, elastin,
CC insulin-like growth factor binding protein-2, alpha-2 type IV collagen,
CC transmembrane receptor PK7, collagen type XVIII alpha 1,
CC platelet derived growth factor receptor alpha, laminin M chain,
CC subtilisin like protein PAC4 or nidogen. The method is useful for
CC initial diagnosis of endometriosis, and also for monitoring progress and
CC treatment of the disease. The present sequence is human fibronectin.
XX
XX
SQ Sequence 2386 AA;

Query Match 99.1%; Score 1984; DB 23; Length 2386;
Best Local Similarity 99.7%; Pred. No. 6.2e-141;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAYYOPHPQPPYGHCVTDSGVVSVGMQWLKTQGNKMLCTCLGNGVSCQETAVTQT 61
DB 291 AAYYOPHPQPPYGHCVTDSGVVSVGMQWLKTQGNKMLCTCLGNGVSCQETAVTQT 350
QY 62 YGNSNGEPCVLFPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDOKYSPCTDHTVLVQT 121
DB 351 YGNSNGEPCVLFPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDOKYSPCTDHTVLVQT 410
QY 122 RGNNSGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTONYADOKFGFCPMAAHEIC 181
DB 411 QGNSNGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTONYADOKFGFCPMAAHEIC 470
QY 182 TTNEGVMYRIGDQMDQOHDMGMMRCTCVNGRGEWTCIAYSQLRDQCIYDDITVYNDT 241
DB 471 TTNEGVMYRIGDQMDQOHDMGMMRCTCVNGRGEWTCIAYSQLRDQCIYDDITVYNDT 530
QY 242 FHKRHEGHMLNCTCGQGRGKWCDPVDCQDSESTGFYQIGDSMEKYHGVRYOCYCY 301
DB 531 FHKRHEGHMLNCTCGQGRGKWCDPVDCQDSESTGFYQIGDSMEKYHGVRYOCYCY 550
QY 302 GRGIGEMHCOPLQTYPSSSGPVEVFTETPSQPNSHPIOW 341
DB 591 GRGIGEMHCOPLQTYPSSSGPVEVFTETPSQPNSHPIOW 630

RESULT 14
AAY28914
ID AAY28914 standard; Protein; 720 AA.
XX
XX AAY28914;
AC
XX
XX 21-SEP-1999 (first entry)
XX
XX Fibronectin protein sequence.
XX

KW Migration stimulatory factor; MSF; cell migration; modulation; human;
KW wound healing; scarring; MSF-alpha; epitope; fibronectin.
XX
XX Homo sapiens.
XX
XX W09931233-A1.
XX
XX 24-JUN-1999.
XX
XX 15-DEC-1998; 98WO-GB03766.
XX
XX 16-DEC-1997; 97GB-0026539.
XX
XX (UYDU-) UNIV DUNDEE.
XX
XX Schor AM, Schor SL;
PI
XX WPI; 1999-430039/36.
XX
XX Proteins with cell migration stimulatory activity used in treating
PT wound and preventing scarring
PT
XX
XX Disclosure; Fig 2; 86pp; English.
XX
XX The invention provides a human migration stimulatory factor (MSF)
CC protein. Host cells containing a replicable vector producing the MSF
CC encoding nucleic acid can be used for the recombinant production of the
CC protein. The polypeptide can be used for modulating cell migration,
CC healing a wound and for preventing scarring. The present sequence
CC represents the human fibronectin.
XX
XX
SQ Sequence 720 AA;

Query Match 98.9%; Score 1979; DB 20; Length 720;
Best Local Similarity 99.4%; Pred. No. 3.8e-141;
Matches 338; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 AAYYOPHPQPPYGHCVTDSGVVSVGMQWLKTQGNKMLCTCLGNGVSCQETAVTQT 61
DB 309 AAYYOPHPQPPYGHCVTDSGVVSVGMQWLKTQGNKMLCTCLGNGVSCQETAVTQT 368
QY 62 YGNSNGEPCVLFPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDOKYSPCTDHTVLVQT 121
DB 369 YGNSNGEPCVLFPFTYNGRTFYSCTTEGRDGHLMCSTTSNYEDOKYSPCTDHTVLVQT 428
QY 122 RGNNSGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTONYADOKFGFCPMAAHEIC 181
DB 429 QGNSNGALCHFPFLYNNHNYTCTSEGRDNNKMGCTTONYADOKFGFCPMAAHEIC 488
QY 182 TTNEGVMYRIGDQMDQOHDMGMMRCTCVNGRGEWTCIAYSQLRDQCIYDDITVYNDT 241
DB 489 TTNEGVMYRIGDQMDQOHDMGMMRCTCVNGRGEWTCIAYSQLRDQCIYDDITVYNDT 548
QY 242 FHKRHEGHMLNCTCGQGRGKWCDPVDCQDSESTGFYQIGDSMEKYHGVRYOCYCY 301
DB 549 FHKRHEGHMLNCTCGQGRGKWCDPVDCQDSESTGFYQIGDSMEKYHGVRYOCYCY 608
QY 302 GRGIGEMHCOPLQTYPSSSGPVEVFTETPSQPNSHPIOW 341
DB 609 GRGIGEMHCOPLQTYPSSSGPVEVFTETPSQPNSHPIOW 648

RESULT 15
AAM63171
ID AAM63171 standard; peptide; 2386 AA.
XX
XX AAM63171;
AC
XX
XX 27-OCT-1998 (first entry)
XX
XX Amino acid sequence of fibronectin.
XX
XX Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
KW

KW tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
 KW antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
 KW hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
 KW inflammatory skin condition; fibronectin.

OS Mus sp.

PN W09833812-A1.

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-US01865.

PR 05-FEB-1997; 97US-0037090.

PA (BGMH) BRIGHAM & WOMENS HOSPITAL.

PI Huang C, Stevens RL;

DR WPI; 1998-437390/37.

PT Tryptase-6 complex inhibitory peptides - used to treat mast
 cell-mediated inflammatory disorders e.g. asthma

PS Disclosure; Pages 36-42; 69pp; English.

CC This is the amino acid sequence of fibronectin. The tryptase-6 complex
 CC inhibitory peptides of the invention comprise the sequence of a fragment
 CC of the fibronectin (residues 1351-1356). Sequences shown in AAM63160 to
 CC AAM63169 represent mouse mast cell protease (mMCP-6) inhibitory
 CC peptides. These peptides which are tryptase-6 complex inhibitors, can be
 CC used for treating a mast cell-mediated inflammatory disorder. The
 CC inhibitors can be used to treat inflammatory disorders including asthma,
 CC allergic rhinitis, urticaria and antioedema, eczematous dermatitis
 CC (atopic dermatitis), anaphylaxis, hyperproliferative skin disease, peptic
 CC ulcers, inflammatory bowel disorder, hyperresponsiveness and inflammatory
 CC skin conditions.

XX SQ Sequence 2386 AA;

Query Match 98.9%; Score 1979; DB 19; Length 2386;

Best Local Similarity 99.4%; Pred. No. 1.5e-140; Indels 0; Gaps 0;

Matches 338; Conservative 1; Mismatches 1;

QY	2	AAVYQPPHPPPPYGHCVTDSGVVYSVMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT	61
DB	291	AAVYQPPHPPPPYGHCVTDSGVVYSVMQMLKTQGNKQMLCTCLGNGVSCQETAVTQT	350
QY	62	YGSNSNGEPCVLPFTYNGRTFYSCCTEGRDGHLWCSTTSNVEDQKYSFCTDHTVLVQT	121
DB	351	YGSNSNGEPCVLPFTYNGRTFYSCCTEGRDGHLWCSTTSNVEDQKYSFCTDHTVLVQT	410
QY	122	RGNSNGALCHFPPLNNHNTTDCSEGRNNMKCGTTQNYDADQKGFPCMAAHEIC	181
DB	411	QGSNSNGALCHFPPLNNHNTTDCSEGRNNMKCGTTQNYDADQKGFPCMAAHEIC	470
QY	182	TTNEGVMYRIQDQDKQDHGMKRCCTCVNGRGEMWTCTIAYSQLRDQCIVDITVNDT	241
DB	471	TTNEGVMYRIQDQDKQDHGMKRCCTCVNGRGEMWTCTIAYSQLRDQCIVDITVNDT	530
QY	242	FHKHBEHGMINTCTCFQGGGRMKCDPVDCQDSETFYQIGDSEKRYHGVRYQCYCY	301
DB	531	FHKHBEHGMINTCTCFQGGGRMKCDPVDCQDSETFYQIGDSEKRYHGVRYQCYCY	590
QY	302	GRGIGEMHCOPLOTYPSSSGPVEVFITTPSQPNSHPIQW	341
DB	591	GRGIGEMHCOPLOTYPSSSGPVEVFITTPSQPNSHPIQW	630

Search completed: November 28, 2003, 15:00:41
 Job time : 46 secs